

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 01:27:42 ; Search time 3689 Seconds

(without alignments)
9947.394 Million cell updates/sec

Title: US-09-811-094-3

Perfect score: 897
Sequence: 1 atgacgagcagcagccatctc.....agctcaagaaggtgatctaa 897

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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37: em_hcg_vrt:*
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40: em_higo_mus:*
41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	100.0	897	6	AX134720
2	897	100.0	897	2	AX301848
3	897	100.0	1399	9	BC031912
4	895.4	99.8	1193	9	BC008935
5	895.4	99.8	1308	9	BC007295
6	895.4	99.8	1344	9	AY007135
7	895.4	99.8	1366	9	BC007850
8	895.4	99.8	1455	9	BC014775
9	895.4	99.8	1466	9	BC008737
10	774.4	86.3	1349	4	BOV1218ANS
11	771.2	86.0	1116	6	AX337175
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14	758.4	84.5	291762	2	AC125887
15	704.6	78.6	169550	5	AL354854
16	618.6	69.0	1286	5	AF506216
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18	605.8	67.5	1194	4	BOV118RANS
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22	596.2	66.5	1215	10	RATANT2
23	594.6	66.3	897	6	AX134719
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29	593	66.1	1142	10	BC003791
30	593	66.1	1236	10	BC004570
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32	593	66.1	1273	10	MM027315
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42	569.8	63.5	309949	2	AC111573
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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO0132876.
ACCESSION AX134720
VERSION AX134720.1 GI:14271237
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Murphy,A.N., Clevenger,W., Wiley,S.E., Andrejev,A.Y., Frigert,L.G.,
Veliciedl,G. and Davis,R.E.
TITLE Compositions and methods for determining interactions of

mitochondrial components, and for identifying agents that alter such interactions
Patent: WO 0132876-A 3 10-MAY-2001;
JOURNAL

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QY	121	GCACAGCAAGAGATATCCCGCCGACAAAGAGATACAAAGGGCATGTGGATCGATATGGCG	180
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RESULT 2					
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LOCUS	Sequence	3 from Patent WO0185944.			
DEFINITION	AX301848				
ACCESSION	AX301848.1	GI:17382905			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
REMARKS					

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	Anderson, C.M., Davis, R.E., Clevenger, W.W., Wiley, S.E., Miller, S.W., Szabo, T.R., Ghosh, S.S., Moos, W.H., Pelly, Y. and Carroll, A.K.	Production of adenine nucleotide translocase (ant), novel ant ligands and screening assays therefor	Patent: WO 0185944-A 3 15-NOV-2001;	MITOKOR (US)
				Location/Qualifiers
				Eukaryota; Metazoa; Choriata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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/mol_type="genomic DNA"
/db_xref="takon:9606"
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Best Local Similarity	100.0%;	Pred. No. 6;	8e-132;	
Matches 897; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Qy	61	ATTCCTCAAGAGGGCGCTGGCTCCGATGAGCGAGGGGTAAACCTGTCTCTGACAGCTCAAC	120
Db	61	ATTCCTCAAGAGGGCGCTGGCTCCGATGAGCGAGGGGTAAACCTGTCTCTGACAGCTCAAC	120
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Db	121	GCGAGCAAGAGATGCGCGCGCGACAAAGAGTACAAAGGGATGTGAACTGATGTTCGGC	180
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Db	181	ATCCCAAGAGAGAGGGGCGTGCTGTCTCTCTCGAGAGGGGCAACTTGGCCACGTTCATGCG	240
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Db	301	GGGGCGCTGGACAAAGACACAGAGTTCGAGAGTACTTTGCGGCGCAACTGGCTCGCGC	360
Qy	361	GGTGCGGCGCGCGCGACCTCGCTGCTGTGTATACCGCTGGATTTGGCAAGACCGCG	420
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Qy	481	CTGGGTAAGATCAACCAAGTCCAGCGGATCCGGGCGCTGTACCAAGGGTTCAGTGTCTCG	540
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RESULT 3
BC031912
LOCUS
DEFINITION
BC031912 1399 bp mRNA linear PRI 26-JUN-2002
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adenine nucleotide translocator), member 6, clone MGC:29984
IMAGE:5141625, mRNA, complete cds.
BC031912
BC031912.1 GI:21594692
MGC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1399)
Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HQSC
Web site: http://www.hqsc.bcm.tmc.edu/cdna/
Contact: amegbcm.tmc.edu
Gunnarite, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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This clone was selected for full length sequencing because it
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1308)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriques, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smallus, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1308)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
REMARK COMMENT
REMARK Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
Info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzyzanski, Keta Kutsche, Oliver Lee, Soo Sen Lee, Victor Lung, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stolt, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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121 GCGAGCAAGCATGCGCGCGCGCAAGCAAGTCAAGAGCATCGTGCATCTGCTCCGC 180
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173 GCGAGCAAGCATGCGCGCGCGCAAGCAAGTCAAGAGCATCGTGCATCTGCTCCGC 232
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421 CTGGCAGCGGAGCTGGGAAAGTCAAGCAGACGCGAGTTCGAGGCGCTGGAGACTCG 480
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473 CTGGCAGCGGAGCTGGGAAAGTCAAGCAGACGCGAGTTCGAGGCGCTGGAGACTCG 532
|||||
481 CTGGTGAAGATCCAAAGTCCGACGCGATCCGGGGCGCTGACCAAGGCTTCAAGTCTCG 540
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533 CTGGTGAAGATCCAAAGTCCGACGCGATCCGGGGCGCTGACCAAGGCTTCAAGTCTCG 592
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593 GTCCAGGCGCATCATCTTACCGGGCGGCTACTTGGCGGTGACATAGGCGCAAGGCG 652
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653 ATGCTCCCGACCCCAAGAAACAGCAGCATCTGCTGATGATGATGATCGGCGAGACCTG 712
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661 ACCGCGCGTGGCGGCGGTGCTCTTCAAGCGTGGCGGGCGGCGCATGATGATG 720
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841 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897

REMARK

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shcherbakov, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Diehl, N.L., Guan, X., Gupta, J., Ho, S.L., Karlins, E., Legaspi, R.,
Lim, M., Meduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantford, S., Thomas, P.J.,
Thompson, E.E., Touchman, J.W., Tsurguev, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 20 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES

source
Location/Qualifiers
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/mol_type="mRNA"
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/clone_id="N1H.MGC.19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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BASE COUNT

287 a 419 c 409 g 251 t

Query Match 99.8%; Score 895.4; DB 9; Length 1366;
Best Local Similarity 99.8%; Pred. No. 1.1e-131;
Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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101 ATGAGCGAAGAGCCATCTCTCGCAAGAGCTTCTGGCGAGAGCATCGCCGCC 160
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221 GCGAGCAGCAGATCGCGCGCGCAAGAGTACAAAGGCGATGTCAGCATGTCGCG 280
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281 ATCCCAAGAGAGCGCGTGGCTCTTCTGGAGGGGCAACCTTCCCAAGCTCATTCG 340

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

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341 TACTTCCCACTCAAGACCTCAACTTCGCTTCAAGAGTAATACAGAGATCTTCTG 400
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401 GGGGGGCTGAGACAGACAGCAGTCTTGAGAGTACTTGGCGGCAACTGGCTCCGGC 460
361 GGTGGGGCGGGCGGCGACCTCCCTGCTGCTGTAACCCGCTGATTTTCCGAACCCGC 420
461 GGTGGGGCGGGCGGCGACCTCCCTGCTGCTGTAACCCGCTGATTTTCCGAACCCGC 520
421 CTGCGACGCGAGCTGGGAAAGTCAGACAGACCGGAGTTCGAGCGCTGGAGACTGC 480
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661 ACGGCGGCTGGCGGCGGTGTGCTTACCCCTTGACAGCGTGGGCGGCGCATGTAGT 720
761 ACGGCGGCTGGCGGCGGTGTGCTTACCCCTTGACAGCGTGGGCGGCGCATGTAGT 820
721 CAGTCCGGGCGCAAGAGAGCTGACATGTACAGCGGCGCTGCTGCTGGAAGAG 780
821 CAGTCCGGGCGCAAGAGAGCTGACATGTACAGCGGCGCTGCTGCTGGAAGAG 880
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841 GGCATGGGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
941 GGCATGGGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 997

RESULT 8
BC014775
LOCUS
DEFINITION
Homo sapiens, similar to solute carrier family 25 (mitochondrial
carrier; adenine nucleotide translocator), member 5, clone
MGC:17525 IMAGE:3458777, mRNA, complete cds.

ACCESSION
BC014775
VERSION
BC014775.1 GI:15928607
SOURCE
MGC.
ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 1455)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:3042 IMAGE:3342722"
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/protein_id="AAH08737.1"
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/translation="MTBOAISPAKDFIAGIAAISKTAIVAPIERVKLLQVOHASKO
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(mitochondrial carrier; adenine nucleotide translocator),
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BASE COUNT
327 a 441 c 425 g 273 t

Query Match
Best Local Similarity 99.8%; Score 895.4; DB 9; Length 1466;
Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 1 ATGACGGAACAGCCATCTCTTCCGCAAGACTTCTTGGCCGAGGATCCGCCGCC 60
Db 89 ATGACGGAACAGCCATCTCTTCCGCAAGACTTCTTGGCCGAGGATCCGCCGCC 148
Query 61 ATCTCCAAAGACGGCGTGGCTCGATCGAGCGGGTCAACCTGCTGTCGAGGTCAGCAG 120
Db 149 ATCTCCAAAGACGGCGTGGCTCGATCGAGCGGGTCAACCTGCTGTCGAGGTCAGCAG 208
Query 121 GCCAGCAGACAGATCGCCCGCAGACAGAGTACAAAGGCGATCGTGAATGATTCGCGC 180
Db 209 GCCAGCAGACAGATCGCCCGCAGACAGAGTACAAAGGCGATCGTGAATGATTCGCGC 268
Query 181 ATCCCCAAGAGAGAGGCGCTGCTGCTTCTGAGAGGGGCAACCTTCCCAAGTCATTCGC 240
Db 269 ATCCCCAAGAGAGAGGCGCTGCTGCTTCTGAGAGGGGCAACCTTCCCAAGTCATTCGC 328
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Query 361 GGTGGGGCGGCGCACTGCTGCTTCTGAGTACCCGCTGGATTTCGCAAGACCGCG 420
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Query 721 CAGTCCGGCGCGAAAGAGACTGACATCATGATACAGGGGCAACCTGATCTTGGAGGANG 780
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Query 841 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
Db 929 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985

RESULT 10
BOV12TRANS
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BOV12TRANS
Bovine ADP/ATP translocase T2 mRNA, complete cds.
M24103.1 J02845
M24103.1 GI:529416
ADP/ATP translocase; translocase.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 1349)
Powell, S.J., Medd, S.M., Runswick, M.J. and Walker, J.E.
Two bovine genes for mitochondrial ADP/ATP translocase expressed
differences in various tissues
Biochemistry 28 (2), 866-873 (1989)

JOURNAL
MEDLINE
PUBMED
COMMENT
On Aug 13, 1994 this sequence version replaced gi:341114.
Original source text: Bos taurus cDNA to mRNA.
Location/Qualifiers
1..1349
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
64..960
/note="The span given is the longest ORF.; T2"
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/product="translocase"
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/db_xref="GI:529417"
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LVKIKSDIRGLYGFENVSVGGIILYRAVGYDITAGMLPDKNTHIIVSWMTAQ
TVAAGVVSYPFDIVRRMMQSGRKADIMYGTVDKWRKIFDEGKAFKFGAMS
NYLRMGCAFVLVLDLKKV"

CDS
242 a 447 c 409 g 251 t

BASE COUNT
242 a 447 c 409 g 251 t

Query Match
Best Local Similarity 86.3%; Score 774.4; DB 4; Length 1349;
Matches 820; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Query 1 ATGACGGAACAGCCATCTCTTCCGCAAGACTTCTTGGCCGAGGATCCGCCGCC 60
Db 64 ATGACGGAACAGCCATCTCTTCCGCAAGACTTCTTGGCCGAGGATCCGCCGCC 123
Query 61 ATCTCCAAAGACGGCGTGGCTCGATCGAGCGGGTCAACCTGCTGTCGAGGTCAGCAG 120
Db 124 ATCTCCAAAGACGGCGTGGCTCGATCGAGCGGGTCAACCTGCTGTCGAGGTCAGCAG 183
Query 121 GCCAGCAGACAGATCGCCCGCAGACAGTACAAAGGCGATCGTGAATGATTCGCGC 180

[illegible][illegible]

ORGANISM	Homio sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	1
AUTHORS	Alvarez,C., Horne,D., Pears-da-Silva,S. and Vockley,J.G.
TITLE	Gene expression profiles in liver cancer
JOURNAL	Patent: WO 0229103-A 2096 11-APR-2002;
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Best Local Similarity	99.2%; Pred. No. 4,3e-112;
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Db	61 GACGCGATGTCGGATCCCAAGGAGAGGGCGTGCCTTGTGAGGGGCAACCTT 120
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OY	346 AACCTGAGCTCCGGGCGGTGCGCGCGCGACGCTCCTCTGCTGTGATCCGCTGGAT 405
Db	238 AACCTGAGCTCCGGGCGGTGCGCGCGCGACGCTCCTCTGCTGTGATCCGCTGGAT 297
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Db	598 CGGCGCATGATGATGCTCCGGGGGCAAGAGAGCTGCATCATGTATACACGGGACCGTGC 657
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QY	886	AAGTGATCTAA	897		
Db	778	AAGTGATCTAA	789		
RESULT 13					
LOCUS	HMNTLCA	1116 bp	RNA	linear	PRI 03-AUG-1993
DEFINITION	Human ADP/ATP translocase mRNA, 3' end, clone pHT8.				
ACCESSION	J03592	GI:339722			
VERSION	J03592.1	GI:339722			
KEYWORDS	ADP/ATP translocase.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1116)				
TITLE	Houldsworth,J. and Attardi,G.				
	Two distinct genes for ADP/ATP translocase are expressed at the				
	mRNA level in adult human liver				
	Proc. Natl. Acad. Sci. U.S.A. 85 (2), 377-381 (1988)				
JOURNAL	88124845				
MEDLINE	2829183				
COMMENT	Original source text: Human (adult) liver, cDNA to mRNA, clone pHT8.				
	Draft entry and printed copy of sequence for [1] kindly provided by J.Houldsworth, 04-JAN-1988.				
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BASE COUNT	231 a 330 c 346 g 209 t				
ORIGIN	5 bp upstream of PstI site.				
Query Match	86.0%	Score 771.2;	DB 9;	Length 1116;	
Best Local Similarity	99.2%	Pred. No. 4.3e-112;			
Matches 786;	Conservative 0;	Mismatches 3;	Indels 3;	Gaps 1;	
QY	106	CTGCAGGTCGACGACGACGAGAACGACGATGCGCGCGACGAACGATCAAGGGCATG	165		
Db	1	CTGCAGGTCGACGACGACGACGATGCGCGCGACGAACGATCAAGGGCATG	60		
QY	166	GACTGCATTTGTGCGCATCCCCAGAGAGAGGCGTGTGTCCTCTTGAGGGGCAACCTT	225		
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QY	226	GCCACAGTCATCTCCCTACTTCCGCCACATCAAGCCCTCAACTTCGCTTCAAGATAACTAC	285		
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QY	286	AAGCAGATCTTCCCTGAGGGGCGTGGACACGACGAGATCTGAGAGTACTTTGGCGGC	345		
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QY	406	TTTCCGCAAGACCCGCTGCGACGCGGACGAGTGGGAAAGTCAGGCACAGACGCGGATTCGGA	465		
Db	298	TTTCCGCAAGACCCGCTGCGACGCGGACGAGTGGGAAAGTCAGGCACAGACGCGGATTCGGA	357		

OY		466	GAGCCGCGGAACATCGCTGGTGAAGATCAACCAGAATCGACGAGCATCCGGGGCGCTGTACAG	525			
Db		358	GAGCCGCGGAACATCGCTGGTGAAGATCAACCAGAATCGACGAGCATCCGGGGCGCTGTACAG	417			
OY		526	GACTTCAGTGTCGTCGTGAGAGGCCATCATATCTACCGGGGGGCCTACTTTGGCGGTGAC	585			
Db		418	GSCCTTAGTGTCGTCGTGAGAGGCCATCATATCTACCGGGGGGCCTACTTTGGCGGTGAC	477			
OY		586	GATTACGGCCAAAGGCGCATGTCCTCCCGACCCCAAAGAAGCAGCANCTGCTGACGTGATG	645			
Db		478	GATTACGGCCAAAGGCGCATGTCCTCCCGACCCCAAAGAAGCAGCATGCTGCTGACGTGATG	537			
OY		646	ATCCGCGAAGACCGTCGACGCGCCGTGGCGGGGTGTCCTACCCCTTGACACGGTGGCG	705			
Db		538	ATCCGCGAAGACCGTCGACGCGCCGTGGCGGGGTGTCCTACCCCTTGACACGGTGGCG	597			
OY		706	CGGCGCATGATGATGTCGATCGCGGGGCGCAAAAGAGCTGACATCATGTACAGGGCACCGTC	765			
Db		658	GACTGTGTGAGGAAGATCTTCCAGAGATGAGGGGGCGCAAGCCCTTCTTTC AAGGCTGGTGG	717			
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OY		718	TTCACAGCTCTCTCGGGGGGATGAGGGGGGCGCCTTGCTGTCGTGCTGTACGACGAGCTCAAG	777			
OY		886	AAGCGATCTTAA 897				
Db		778	AAGCGATCTTAA 789				
RESULT 14							
AC125887/C							
LOCUS							
DEFINITION			Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS				
ACCESSION			AC125887	291762 bp DNA linear HTG 15-NOV-2002			
VERSION			AC125887.3	GI:25008671			
KEYWORDS			HTG; HNGS PHASE1; HNGS_DRAFT; HNGS_ENRICHED.				
SOURCE			Rattus norvegicus (Norway rat)				
ORGANISM			Rattus norvegicus				
REFERENCE							
AUTHORS			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Natus;				
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TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

2 (bases 1 to 291762)
Unpublished
Direct Submission

Worley, K.C.
Submitted Submission
Submitted (02-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 291762)
Rat Genome Sequencing Consortium.
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced g1:23269681.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/atl/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GMDL
Center clone name: CH230-274J3
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 226053 bases at least Q40
Consensus quality: 230853 bases at least Q30
Consensus quality: 233473 bases at least Q20
Estimated insert size: 233445; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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*	95032	95131:	gap of unknown length
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*	109057	271697:	contig of 162641 bp in length
*	271698	271797:	gap of unknown length
*	271798	273026:	contig of 1229 bp in length
*	273027	273126:	gap of unknown length
*	273127	274531:	contig of 1405 bp in length
*	274532	274631:	gap of unknown length
*	274632	276587:	contig of 1656 bp in length
*	276588	276587:	gap of unknown length
*	276388	277904:	contig of 1517 bp in length
*	276388	277905:	gap of unknown length
*	277905	278004:	gap of unknown length
*	278005	279523:	contig of 1519 bp in length
*	279524	279633:	gap of unknown length
*	279624	280724:	contig of 1101 bp in length
*	280725	280824:	gap of unknown length
*	280825	284658:	contig of 3834 bp in length
*	284659	284758:	gap of unknown length
*	284759	287324:	contig of 2476 bp in length
*	287235	287334:	gap of unknown length
*	287335	291762:	contig of 4428 bp in length.

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ORIGIN

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QY	481	CTGGTAAAGATCAACCAAGTCCAGCGGCATCCGGGGCTGTACCAAGGGCTTCAGTGTCTCC	540
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QY	541	GTCCAGGGCATCATCTTACCGGGGGGCGCTACTTGGCGCTGACATACGGCCAAAGGC	600
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QY	601	ATGCTCCCGACCCCAAGAACACGACGACATCGTGTAGCTGATGATCGCAGACCGTG	660
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QY	661	ACGGCCGTGGCCGGCGGTGTGTCTTACCCCTTGACACGCTGCGCGGGCGCATGATGATG	720
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QY	721	CAGTCCGGGGCAAAGAGACTGATCATGTATACGGGGA	760
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RESULT	15
LOCUS	ALJ354854
DEFINITION	ALJ354854 169550 bp DNA linear PRI 21-OCT-2001
ACCESSION	Human DNA sequence from clone RP11-572H4 on chromosome 9, complete sequence.
VERSION	ALJ354854
KEYWORDS	ALJ354854.8 GI:15131220
SOURCE	HTG.
ORGANISM	Homo sapiens (human)
TITLE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Etheria; Primates; Carniphini; Homnidae; Homo. Clark,G.
JOURNAL	Direct Submission Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Aug 9, 2001 this sequence version replaced gi:14625557.
COMMENT	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 00:45:07 ; Search time 314 Seconds

(without alignments)
7111.452 Million cell updates/sec

Title: US-09-811-094-3

Perfect score: 897
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	897	100.0	897	21	AAD00521	Human adenine nucl
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4	895.4	99.8	1212	22	AAI58797	Human polynucleoti
5	895.4	99.8	2035	22	AAI60583	Human polynucleoti
6	873.4	97.4	2592	25	ABX63152	Human cdna #152 di
7	816.4	91.0	2213	25	ACC46652	Human ditlp organe
8	771.2	86.0	1116	24	ABK83761	Human cdna differe

9	771.2	86.0	1116	24	ABN95598	Gene #2096 used to
10	771.2	86.0	1116	24	ABL69347	Prostate cancer re
11	647.4	72.2	687	24	ABO56282	Human ovarian anti
12	596.2	66.5	1196	24	ABK63420	Rat sequence diffe
13	596.2	66.5	1225	24	AAI48635	Human insulin rece
14	594.6	66.3	897	21	AAD00520	Human adenine nucl
15	594.6	66.3	897	22	AAS05902	Human adenine nucl
16	594.6	66.3	897	22	AAS16689	DNA encoding human
17	591.4	65.9	1259	19	AAV36480	Ant1 CDNA. Mus sp
18	588.2	65.6	1177	19	AAV36479	Ant1 CDNA. Mus sp
19	568.4	63.4	1156	23	AAV36479	DNA encoding novel
20	564.2	62.9	894	21	AAD00519	Human adenine nucl
21	564.2	62.9	894	22	AAS05901	Human adenine nucl
22	564.2	62.9	894	22	AAS16688	DNA encoding human
23	564.2	62.9	1024	25	ABZ83302	Toxicologically re
24	564.2	62.9	1320	24	ABS56029	Invertebrate forag
25	550.4	61.4	669	24	ABZ33737	Human TRICH encodi
26	519.2	57.9	1581	23	ABL18531	Drosophila melanog
27	519.2	57.9	1750	23	ABL20967	Drosophila melanog
28	482.4	53.8	2706	22	AAS29836	Human cytoskeletal
29	482.4	53.8	2706	22	AAS35083	DNA #33 encoding h
30	482.4	53.8	220895	24	ABK84798	Human cdna differe
31	462.6	51.6	1033	23	ABL03127	Drosophila melanog
32	406.6	45.3	943	24	ABN74319	Human TRICH_19 CDN
33	400.8	44.7	1251	23	AAS79610	DNA encoding novel
34	394	43.9	720	24	ABZ76857	Frog embryonic gen
35	394	43.9	720	24	ABZ76857	Frog embryonic gen
36	363	40.5	4545	23	AAS68190	DNA encoding novel
37	354.4	39.5	1781	24	AAD33664	Human TRICH_19 CDN
38	354.4	39.5	1803	23	ABX71399	Human metabolism-a
39	344.6	38.4	5407	23	ABL18530	Drosophila melanog
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41	338.8	37.8	639	24	ABT09322	Phase-1 Rat CT gen
42	332.2	37.0	988	24	ABN74435	Bovine embryonic g
43	325.8	36.3	5768	24	ABL61797	Colon adenocarcino
44	322.6	36.0	731	20	AAK39617	Breast cancer asso
45	318.6	35.5	434	25	ABX47259	Bovine EST associa

ALIGNMENTS

RESULT 1	
ID	AAD00521 standard; cdna: 897 BP.
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AC	AAD00521;
XX	
DT	29-AUG-2000 (first entry)
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DE	Human adenine nucleotide translocator ANT3 CDNA.
KW	Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotoxic;
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dysostia;
KW	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome; ss.
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FT	CDS
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PD	11-MAY-2000.

XX 03-NOV-1999; 99MO-US25883.
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 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS;
 DR MPI: 2001-365619/31.
 XX F-PSDB; AAT171033.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT against mitochondrial disease -
 XX
 PS Example 1: Page 166; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA
 CC encoding adenine nucleotide translocator ANT3 from human brain.
 XX
 SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other;
 Query Match 100.0%; Score 897; DB 21; Length 897;
 Best Local Similarity 100.0%; Pred. No. 1.3e-175;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 OY 481 CTGGTGAAGATCACCAGATCCGAGGCGATCCGGGGCCGTGTACAGAGGCTTCATGTCTCC 540
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 DB 721 CAGTCCGGGCGCAAGAGAGCTGACATCATGTACAGGGGACCGTGTGAGAGGAAG 780
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 ID AAS05903
 XX AAS05903;
 AC
 XX
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-3 (ANT-3) cDNA sequence.
 XX
 DE Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 PN WO200132876-A2.
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 PD 10-MAY-2001.
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 PF 03-NOV-2000; 2000MO-US30535.
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 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Erliger LG;
 PI Velicelebi G, Davis RE;
 DR MPI: 2001-291054/30.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide

PT fused to energy transfer molecule -
 PS Disclosure; Fig 1; 186bp; English.
 XX
 CC The present sequence encodes for human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX

Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other;

Query Match 100.0%; Score 897; DB 22; Length 897;
 Best Local Similarity 100.0%; Pred. No. 1.3e-175;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGGAACAGCCATCTCTTCCGCAAGACCTTTGGCGGAGCATCCGCCGCC 60
 DB 1 ATGAGCGGAACAGCCATCTCTTCCGCAAGACCTTTGGCGGAGCATCCGCCGCC 60
 QY 61 ATCTCCAAAGACGGCGCTGCTCCGATCGAGCGGGTCAAGCTGCTGCAAGTCCGAC 120
 DB 61 ATCTCCAAAGACGGCGCTGCTCCGATCGAGCGGGTCAAGCTGCTGCAAGTCCGAC 120
 QY 121 GCCAGCAAGACAGATGCGCGCCGACAAAGATCAAGGGCATGTGATCTTGTCCG 180
 DB 121 GCCAGCAAGACAGATGCGCGCCGACAAAGATCAAGGGCATGTGATCTTGTCCG 180
 QY 121 GCCAGCAAGACAGATGCGCGCCGACAAAGATCAAGGGCATGTGATCTTGTCCG 180
 DB 121 GCCAGCAAGACAGATGCGCGCCGACAAAGATCAAGGGCATGTGATCTTGTCCG 180
 QY 181 ATCCCAAGAGAGAGGGGCTGCTCTTCTGAGGGGCAACCTTCCAACTCATTCGC 240
 DB 181 ATCCCAAGAGAGAGGGGCTGCTCTTCTGAGGGGCAACCTTCCAACTCATTCGC 240
 QY 181 ATCCCAAGAGAGAGGGGCTGCTCTTCTGAGGGGCAACCTTCCAACTCATTCGC 240
 DB 181 ATCCCAAGAGAGAGGGGCTGCTCTTCTGAGGGGCAACCTTCCAACTCATTCGC 240
 QY 241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGATAGACAGAGATCTTCG 300
 DB 241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGATAGACAGAGATCTTCG 300
 QY 301 GGGGGCGTGACACACACAGATTCGAGGTACTTGGCGGCAACCTTGGCTCCGCG 360
 DB 301 GGGGGCGTGACACACACAGATTCGAGGTACTTGGCGGCAACCTTGGCTCCGCG 360
 QY 361 GGTGGCGGGCGGCGACCTCTCTGCTTGTGATCCGCTGGATTTGCCAGAACCCGC 420
 DB 361 GGTGGCGGGCGGCGACCTCTCTGCTTGTGATCCGCTGGATTTGCCAGAACCCGC 420
 QY 421 CTGGCAGCGGAGCTGGGAAAGTCAGGACAGACCGGAGTTCGAGGCGCTGGAGACTGC 480
 DB 421 CTGGCAGCGGAGCTGGGAAAGTCAGGACAGACCGGAGTTCGAGGCGCTGGAGACTGC 480
 QY 481 CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 DB 481 CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 QY 541 GTGCAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 DB 541 GTGCAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 QY 541 GTGCAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 DB 541 GTGCAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGAGGCTTCAAGTCTCC 540
 QY 601 ATGCTCCCGACCCCAAGAACACGACATCGTGTGATGGATGATCCGCGACGCGTG 660
 DB 601 ATGCTCCCGACCCCAAGAACACGACATCGTGTGATGGATGATCCGCGACGCGTG 660

QY 661 ACGGCGGTGGCGCGCTGTGCTTACCCCTTCGACACGTGGCGGCGCATGATGATG 720
 DB 661 ACGGCGGTGGCGCGCTGTGCTTACCCCTTCGACACGTGGCGGCGCATGATGATG 720
 QY 721 CAGTCCGGGCGCAAGAGACTGACATCATGATACAGCGGACCGTGCATCTTTGAGGAAG 780
 DB 721 CAGTCCGGGCGCAAGAGACTGACATCATGATACAGCGGACCGTGCATCTTTGAGGAAG 780
 QY 781 ATCTTCAGAGATGAGGGGGCAAGGCGCTTCTTCAAGGGTGGCGTCAAGCTCCGCGG 840
 DB 781 ATCTTCAGAGATGAGGGGGCAAGGCGCTTCTTCAAGGGTGGCGTCAAGCTCCGCGG 840
 QY 841 GGCATGGGGGGCGCTTCTGCTGCTGTACAGACAGCTCAAGAGGTGATCTAA 897
 DB 841 GGCATGGGGGGCGCTTCTGCTGCTGTACAGACAGCTCAAGAGGTGATCTAA 897

RESULT 3

AA16690 standard; cDNA; 897 BP.
 AA16690;

14-FEB-2002 (first entry)

DNA encoding human adenine nucleotide translocator 3 (ANT3).

Human: adenine nucleotide translocator; ANT; ss;

mitochondrial matrix protein.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..897 /tag= a

FT /product= "adenine nucleotide translocator 3 (ANT3)"

PN MO200185944-A2.

PD 15-NOV-2001.

XX 11-MAY-2001; 2001MO-US15416.

XX 11-MAY-2000; 2000US-0569327.

PR (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Cleveanger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;

XX WPI: 2002-055598/07.

DR P-PSDB; AAU10380.

XX Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide

XX Example 3; Fig 1; 147bp; English.

XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. CC The present sequence represents the coding sequence of human ANT3. XX

SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other:

Query Match 100.0%; Score 897; DB 24; Length 897; Best Local Similarity 100.0%; Pred. No. 1.3e-175;

Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTCTTGGCCGAGGAGCATCCGCGCCG 60
1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTCTTGGCCGAGGAGCATCCGCGCCG 60
61 ATCTCCAAAGACGCGCGCTGCTCGATCCAGCGGGGTCAAGCTGCTGCTGAGAGTCTTCC 120
61 ATCTCCAAAGACGCGCGCTGCTCGATCCAGCGGGGTCAAGCTGCTGCTGAGAGTCTTCC 120
121 GCCAGCAAGCAGATCGCGCCGACAAAGACATCTGAGACTGATCTTCCG 180
121 GCCAGCAAGCAGATCGCGCCGACAAAGACATCTGAGACTGATCTTCCG 180
181 ATCCCAAGAGACAGGCGCTGCTCTCTTGTGAGAGGGCAACCTTCCAACTTCG 240
181 ATCCCAAGAGACAGGCGCTGCTCTCTTGTGAGAGGGCAACCTTCCAACTTCG 240
241 TACTTCCCACTCAAGCCCTCAACTTTCGCTTCAAGGATTAAGTACAAGAGATCTTCTG 300
241 TACTTCCCACTCAAGCCCTCAACTTTCGCTTCAAGGATTAAGTACAAGAGATCTTCTG 300
301 GGGGCGGTGACAAAGCAGACAGCTTGTGAGAGTACTTGTGGGGCAACCTGCGCG 360
301 GGGGCGGTGACAAAGCAGACAGCTTGTGAGAGTACTTGTGGGGCAACCTGCGCG 360
361 GGTGCGCGCGCGGACATCTCTCTGCTGCTGACCGCGGATTTTTCGCAAGACCGCG 420
361 GGTGCGCGCGCGGACATCTCTCTGCTGCTGACCGCGGATTTTTCGCAAGACCGCG 420
421 CTGGAGAGGACGCTGGGAAAGTCAAGCAAGAGCGGCGGATTCGAGAGCCCTGGGAA 480
421 CTGGAGAGGACGCTGGGAAAGTCAAGCAAGAGCGGCGGATTCGAGAGCCCTGGGAA 480
481 CTGGGAAAGTCAACCAAGTCCAGCGCATCCGCGCGCTTACAGGCTTCAAGTCTCC 540
481 CTGGGAAAGTCAACCAAGTCCAGCGCATCCGCGCGCTTACAGGCTTCAAGTCTCC 540
541 CTGGAGGCGCATCATCTACCGGCGCGCTTACCTTCCGCTGACATACGCGCAAGGCG 600
541 CTGGAGGCGCATCATCTACCGGCGCGCTTACCTTCCGCTGACATACGCGCAAGGCG 600
601 ATGCTCCCGCCAGCCCAAGACAGCAGCATCTGTGTGAGCTGATGATGCGCAGACCTG 660
601 ATGCTCCCGCCAGCCCAAGACAGCAGCATCTGTGTGAGCTGATGATGCGCAGACCTG 660
661 ACGGCGGTGCGCGCGGTGTCTACCCCTTGCACAGGCTGCGGGGCGCATGATGATG 720
661 ACGGCGGTGCGCGCGGTGTCTACCCCTTGCACAGGCTGCGGGGCGCATGATGATG 720
721 CAGTCCGCGGCAAAAGAGCTGATCATGTACACGCGGCACTGCTGTGAGAGAG 780
721 CAGTCCGCGGCAAAAGAGCTGATCATGTACACGCGGCACTGCTGTGAGAGAG 780
781 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGGTTCGCTGCTCAAGCTCTGCGG 840
781 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGGTTCGCTGCTCAAGCTCTGCGG 840
841 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
841 GGCATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

RESULT 4

AA158797
ID AA158797 standard; cDNA; 1212 BP.
AC AA158797;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 1000.

XX Human; nototropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX Leukaemia; ss.

XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX
XX 25-APR-2000; 2000US-0552317.
XX
XX 09-JUL-2000; 2000US-0598042.
XX
XX 19-JUL-2000; 2000US-0620312.
XX
XX 03-AUG-2000; 2000US-0653450.
XX
XX 14-SEP-2000; 2000US-0662191.
XX
XX 19-OCT-2000; 2000US-0693036.
XX
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao Q, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX
XX P-PSDB: AAM39641.

XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 1000; 1007bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nototropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.

SQ Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 other:

Query Match 99.8%; Score 895.4; DB 22; Length 1212;
Best Local Similarity 99.9%; Pred. No. 2.8e-175;

Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTCTTGGCCGAGGAGCATCCGCGCCG 60
131 ATGACGGAACAGGCGCATCTCTTGGCCAAAGACTTCTTGGCCGAGGAGCATCCGCGCCG 190

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QY 61 ATCTCAAGAGCGCGGTGCTCCATGACGCGGTGCAAGCTGCTGTCAGTCCAGCAC 120
   |||
Db 191 ATCTCAAGAGCGCGGTGCTCCATGACGCGGTGCAAGCTGCTGTCAGTCCAGCAC 250
QY 121 GCCAGCAAGAGATGCGCGCGGACAGAGTACAGAGGCAATGCTGATGCTGTCGCG 180
   |||
Db 251 GCCAGCAAGAGATGCGCGCGGACAGAGTACAGAGGCAATGCTGATGCTGTCGCG 310
QY 181 ATCCCAAGAGAGAGCGGTGCTGCTGCTGAGAGGCGCAACCTTGCCAACTGATTCGC 240
   |||
Db 311 ATCCCAAGAGAGAGCGGTGCTGCTGCTGAGAGGCGCAACCTTGCCAACTGATTCGC 370
QY 241 TACTTCCCACTCAAGCCCTCACTTGCCTTCAAGATTAAGTACAGAGATGCTTCCTG 300
   |||
Db 371 TACTTCCCACTCAAGCCCTCACTTGCCTTCAAGATTAAGTACAGAGATGCTTCCTG 430
QY 301 GGGGGCGTGGACACACAGCATGTTGAGAGTACTTGGCGGCAACTGGCTCCGCG 360
   |||
Db 431 GGGGGCGTGGACACACAGCATGTTGAGAGTACTTGGCGGCAACTGGCTCCGCG 490
QY 361 GGTGCGCGCGCGCGACCTCCCTGCTGCTGCTGACCGCGTGGATTTTGGCAACCGCG 420
   |||
Db 491 GGTGCGCGCGCGCGACCTCCCTGCTGCTGCTGACCGCGTGGATTTTGGCAACCGCG 550
QY 421 CTGCGACGCGAGCTGGGAAAAGTCAAGACACAGCGCGAGTTCCGAGGCGTGGAGACTGC 480
   |||
Db 551 CTGCGACGCGAGCTGGGAAAAGTCAAGACACAGCGCGAGTTCCGAGGCGTGGAGACTGC 610
QY 481 CTGCGAAGATCACCAAGTCCGACGCGCATCCGCGGCGCTGACAGAGGCTGATGCTCTGC 540
   |||
Db 611 CTGCGAAGATCACCAAGTCCGACGCGCATCCGCGGCGCTGACAGAGGCTGATGCTCTGC 670
QY 541 GTGACGGGCATCATCATCTACCGGGCGGCTACTTCCGCGGTGATGATGACGCGCAAGGCG 600
   |||
Db 671 GTGACGGGCATCATCATCTACCGGGCGGCTACTTCCGCGGTGATGATGACGCGCAAGGCG 730
QY 601 ATGCTCCCGGACCCCAAGAACACGACATGCTGAGTGTGATGATGCGCGACAGCCGTG 660
   |||
Db 731 ATGCTCCCGGACCCCAAGAACACGACATGCTGAGTGTGATGATGCGCGACAGCCGTG 790
QY 661 ACGGCGTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
   |||
Db 791 ACGGCGTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
QY 721 CAGTCCGCGCGCAAGAGAGTACATGATGACAGCGCGCGTGCATGCTGTTGAGAGAG 780
   |||
Db 851 CAGTCCGCGCGCAAGAGAGTACATGATGACAGCGCGCGTGCATGCTGTTGAGAGAG 910
QY 781 ATCTTCAAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGCTCAACGCTGCGG 840
   |||
Db 911 ATCTTCAAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGCTCAACGCTGCGG 970
QY 841 GGCATGGGGGGGCGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
   |||
Db 971 GGCATGGGGGGGCGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1027

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RESULT 5
AA160583/c
ID AA160583 standard: cDNA: 2035 BP.

AA160583:

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4572.

Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

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KW 1 leukemia; ss.
OS Homo sapiens.
PN WO200153312-A1.
PD 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
PF 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0596042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou P, Goodrich R, Dymnac RT;
XX WPI: 2001-442253/47.
DR P-PSDB: AAM41427.
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PS Claim 1; SEQ ID NO 4572; 10078bp; English.
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX Sequence 2035 BP; 398 A; 611 C; 625 G; 401 T; 0 other;
SQ

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Query Match 99.8%; Score 895.4; DB 22; Length 2035;
Best Local Similarity 99.9%; Pred. No. 3e-175;
Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATGACGGAACAGGCGCATCTCTTCCCAAGACTTCTTGGCGGAGCATCCCGCGCG 60
   |||
Db 1932 ATGACGGAACAGGCGCATCTCTTCCCAAGACTTCTTGGCGGAGCATCCCGCGCG 1873
QY 61 ATCTCCAGAGCGCGGTGCTCGATGACGCGGGTCAAGCTGCTGCTGACGATCCAGCAC 120
   |||
Db 1872 ATCTCCAGAGCGCGGTGCTCGATGACGCGGGTCAAGCTGCTGCTGACGATCCAGCAC 1813
QY 121 GCGAGCAAGCAATGCGCGCGGACAGAGTACAGAGGATGATGATGATGATGATGATGATG 180
   |||
Db 1812 GCGAGCAAGCAATGCGCGCGGACAGAGTACAGAGGATGATGATGATGATGATGATGATG 1753
QY 181 ATCCCAAGAGAGAGCGGTGCTGCTGCTGCTGAGGCGCAACTTGCACATGATTCGC 240
   |||
Db 1752 ATCCCAAGAGAGAGCGGTGCTGCTGCTGCTGAGGCGCAACTTGCACATGATTCGC 1693
QY 241 TACTTCCCACTCAAGCCCTCACTTGCCTTCAAGATTAAGTACAGAGATGCTTCCTG 300

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Db	1692	TACTTTCGCCCTCAAGACCCTCAACTTCGCTTCAGAGTAAGTACAGACGAGATCTTCCG	1633
Oy	301	GGGGGGCGTGACACACACACAGCAGTTCCTTGAGGTACTTGGGGCAACCTGGCTCCGGC	360
Db	1632	GGGGCGCGTGGACACAGACACAGCAGTTCCTTGAGGTAAGTTCCTGGGGCAACCTGGCTCCGGC	1573
Oy	361	GGTCCGGCGCGGGCGACACCTCCCTCGTGGTGGTGAACCGCGTGGATTTGGCAGAACCGC	420
Db	1572	GGTCCGGCGCGGGCGACACCTCCCTCGTGGTGGTGAACCGCGTGGATTTGGCAGAACCGC	1513
Oy	421	CTGGGACACCGAGCGTGGGAAATGCAGAGACAGACCGAGATTCGAGGCGTGGAGACTGC	480
Db	1512	CTGGGACACCGAGCGTGGGAAATGCAGAGACAGACCGAGATTCGAGGCGTGGAGACTGC	1453
Oy	481	CTGGTGAAGATCACCAAGTCCGATCCGGGGCGCTACTTGGCGTGTACGATACGCCAAGGCG	600
Db	1452	CTGGTGAAGATCACCAAGTCCGATCCGGGGCGCTACTTGGCGTGTACGATACGCCAAGGCG	1393
Oy	541	GTGCAGGGCATCATCTATCTACCGGGCGGCTACTTGGCGTGTACGATACGCCAAGGCG	600
Db	1392	GTGCAGGGCATCATCTATCTACCGGGCGGCTACTTGGCGTGTACGATACGCCAAGGCG	1333
Oy	601	ATGCTCCCCACACCCCAAGACACGACACATGTCGTGAGTGGATGATTCGGCGACAGCCGTG	660
Db	1332	ATGCTCCCCACACCCCAAGACACGACACATGTCGTGAGTGGATGATTCGGCGACAGCCGTG	1273
Oy	661	ACGGCCCTGGCCCGGCTGGTGTCTTACCCCTTTCGACACGGTGCAGCGGCGCATGATGATG	720
Db	1272	ACGGCCCTGGCCCGGCTGGTGTCTTACCCCTTTCGACACGGTGCAGCGGCGCATGATGATG	1213
Oy	721	CAGTCCGGGGCGCAAGAGACTGATCATGTATACACGGGACCGCTCGACTTTGGAGAGAG	780
Db	1212	CAGTCCGGGGCGCAAGAGACTGATCATGTATACACGGGACCGCTCGACTTTGGAGAGAG	1153
Oy	781	ATCTTCAGAGATGAGGGGGCGCAAGGCCCTTTCGAAGGGTGCCTGGTCCACAGTCTGCGG	840
Db	1152	ATCTTCAGAGATGAGGGGGCGCAAGGCCCTTTCGAAGGGTGCCTGGTCCACAGTCTGCGG	1093
Oy	841	GGCATTGGGGGGCGCTTCGCTGCTGCTGTAGAGAGAGCTCAAGAGTGAATCTAA	897
Db	1092	GGCATTGGGGGGCGCTTCGCTGCTGCTGTAGAGAGAGCTCAAGAGTGAATCTAA	1036
RESULT 6			
ABX63152			
ID ABX63152 standard; cDNA; 2592 BP.			
ABX63152;			
25-FEB-2003 (first entry)			
Human cDNA #152 differentially expressed in activated vascular tissue.			
Human; gene; ss; vascular tissue; cytostatic; atherosclerosis;			
cardiac; hypotensive; antidiabetic; gynaecological; vasotropic;			
cerebroprotective; gene therapy; vascular disease; cancer; coronary;			
artery disease; hypertension; diabetes; pre-eclampsia; restenosis;			
ischaemia-reperfusion injury; stroke;			
Homo sapiens.			
US2002137081-A1.			
26-SEP-2002.			
08-JAN-2002; 2002US-0044090.			
28-JUL-2000; 2000US-222459P.			
08-JAN-2001; 2001US-260483P.			
(BAND/) BANDMAN O.			

P1	Bandman O;
X1	DR
XX	WPI: 2003-110597/10.
PT	Combination for diagnosing, staging, treating, or monitoring the
PR	progression of treatment of a vascular disease, e.g. atherosclerosis,
PT	comprises several cDNAs that are differentially expressed in activated
PS	vascular tissue -
XX	
PS	claim 1; Page -: 18pp; English.
CC	This invention relates to a combination comprising several cDNAs that
CC	are differentially expressed in activated vascular tissue. The invention
CC	also discloses a high throughput method for detecting differentially
CC	expressed cDNAs in a sample. The cDNAs of the invention may have
CC	antiatherosclerotic; cytostatic; cardiant; hypotensive; antiplatelet;
CC	gynecological; vasotropic and cerebroprotective activities and may be
CC	used in gene therapy. The cDNAs of the invention may be used in a
CC	high-throughput methods for detecting differential expression of one or
CC	more cDNAs in a sample, or screening several molecules or compounds to
CC	identify a molecule or compound by the cDNA may be used to screen several
CC	molecules. A protein encoded by the cDNA may be used to detect specific
CC	the protein, or to produce or purify an antibody to the protein that can
CC	be used to detect a protein in a sample or purify a natural or
CC	recombinant protein from a sample. The nucleotides may be useful for
CC	diagnosing, staging, treating, or monitoring the progression of
CC	treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
CC	artery disease, hypertension, diabetes, pre-eclampsia, ischemia-
CC	reperfusion injury, restenosis, or stroke. The cDNAs can also be used
CC	for large-scale genetic or gene expression analysis of several new
CC	nucleic acid molecules. Antibodies to the proteins encoded by the
CC	cDNAs are useful for diagnosing pre-pathologic disorders, and chronic
CC	or acute diseases associated with abnormalities in the expression
CC	amount or distribution of the protein. The present sequence
CC	represents a cDNA of the invention that is differentially expressed in
CC	activated vascular tissue.
CC	Note: The sequence data for this patent did not form part of the
CC	specification, but was obtained in electronic format directly from USPRO
CC	at http://seqdata.uspto.gov/sequence.html?docid=20020137081.
XX	
SQ	Sequence 2592 BP; 520 A; 790 C; 766 G; 514 T; 2 other:
Best Match	97.4%; Score: 873.4; DB 25; Length 2592;
Query Similarity	99.7%; Pcod. No. 1e-170; 1; Indels 2; Gaps 2;
Matches	966; conservative 0; Mismatches 1
OY	1 ATGACGAAAGGCCATCTCCTTGGCCCAAGACTTTGGCGGAGGCAT-CGCGCGGC 59
DB	207 ATGAGCGAAGACGGCATCTTCCTTGCCCAAGACTTTGTGGCCGAGGATGCCCGCCG 266
OY	60 CATCTCCAGAGCGCCGTGGCTGCAGTCAGAC-GGGTCAAAGTGTGCTGAGATGCAC 118
DB	267 CATCTCCAAAGCGCCGTGGCTGCAGTCAGACGGGGCCAAGTGTGCTGAGAGGTCCAG 326
OY	119 ACGCCAGCAAGCAGATGCGCCGCGACAAGCAAGTCAAGGGCATCTGGATGCTATTGTCC 178
DB	327 ACGCCAGCAAGCAGATGCGCGCGACAAGCGGTCAAGGGCATCTGTGATGCTATTGTCC 386
OY	179 GCATCCCCAAGAGAGAGGCGTGTCTCTTCTTGAGGGGCAACCTTGCACAGTCATTTC 238
DB	387 GCATCCCCAAGAGAGAGGCGTGTCTCTTCTTGAGGGGCAACCTTGCACAGTCATTTC 446
OY	239 GCTATTCTCCCACTCAAGGCTCTCATCTTGGCTTCAAGAATAAGTACAGAGCATCTTCC 298
DB	447 GCTATTCTCCCACTCAAGGCTCTCATCTTGGCTTCAAGAATAAGTACAGAGCATCTTCC 506
OY	299 TTGGGGGGGTGGGAACAAGCACAGCATGTTCTGGAGAGTAATTTCGCGGCAACTGGCCCTCC 358
DB	507 TTGGGGGGGTGGGAACAAGCACAGCATGTTCTGGAGAGTAATTTCGCGGCAACTGGCCCTCC 566
OY	359 GCGGTTCGGCGCGCGGAGCACTCGCTCTGTCTGATACCCTGTGATTTGCCAGAACCC 418

Db 567 GCGTGGCGCGCGCGCGACCTCCCTGCTGCTACCCGCTGGATTTTGCACAGACC 626
 Qy 419 GCGTGGCGCGCGCGCGCGAGAGTGCACAGACGCGAGTTCGAGGCTGGAGACT 478
 Db 627 GCGTGGCGCGCGCGCGAGAGTGCACAGACGCGAGTTCGAGGCTGGAGACT 686
 Qy 419 GCGTGGTAAAGTATCAACCAAGTCCGACGGCATCCGGGGCTGTACCAAGGCTTCAGTGTCT 538
 Db 687 GCGTGGTAAAGTATCAACCAAGTCCGACGGCATCCGGGGCTGTACCAAGGCTTCAGTGTCT 746
 Qy 539 CCGTGCAGGCGCATCATCATCTATCTATCTGCGGCGCTGTACGATACGATGCGCAAGG 598
 Db 747 CCGTGCAGGCGCATCATCATCTATCTGCGGCGCTGTACGATACGATGCGCAAGG 806
 Qy 599 GCATGCTCCCGCAGCCCAAGAACACGACGACATGCTGTAGTGAAGTATGATGCGCAGACCG 658
 Db 807 GCATGCTCCCGCAGCCCAAGAACACGACGACATGCTGTAGTGAAGTATGATGCGCAGACCG 866
 Qy 659 TGACGCGCGGTGGCGCGCGTGTCTCTACCCCTTGACACAGGTGGCGGCGCATGATGA 718
 Db 867 TGACGCGCGGTGGCGCGCGTGTCTCTACCCCTTGACACAGGTGGCGGCGCATGATGA 926
 Qy 719 TGCAATCCGCGCGCGCAAGAGAGCTGATCATGTATACAGGCGCACCGTGCATGTTGGAGGA 778
 Db 927 TGCAATCCGCGCGCGCAAGAGAGCTGATCATGTATACAGGCGCACCGTGCATGTTGGAGGA 986
 Qy 779 AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGCGTGTCTCAACGTCCTGCG 838
 Db 987 AGATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGCGTGTCTCAACGTCCTGCG 1046
 Qy 839 GGGGCGATGGGGGGCGCTTCTGCTGTCTCTATACAGAGCTCAAGAGGTGATCTTA 897
 Db 1047 GGGGCGATGGGGGGCGCTTCTGCTGTCTCTATACAGAGCTCAAGAGGTGATCTTA 1105
 RESULT 7
 ACC46652
 ID ACC46652 standard; cDNA; 2213 BP.
 XX
 AC ACC46652;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human dlthp organelle-associated protein-encoding cDNA.
 XX
 KW Human; dlthp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW gene therapy; antisense therapy; drug screening; proteome analysis;
 KW disease model; toxicological testing; genotyping; transgenic animal; knock in;
 KW organelle-associated protein; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297031-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 27-MAR-2002; 2002WO-US10056.
 XX
 XX 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.
 PR 20-JUN-2001; 2001US-300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.

XX Dafo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daubert SC, Dam TC, Liu TF, Nguyen AD, Kleeferd Y, Gerstin EH;
 PI Perilla CH, David MH, Lewis SA, Chen AJ, Penzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RT, Urashka ME;
 DR WPI: 2003-129518/12.
 DR P-PSDB; ABR41715.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for
 PT identifying test compound which specifically binds to a polypeptide
 PT encoded by human diagnostic and therapeutic polynucleotide, and to
 PT induce antibodies
 PS
 XX
 XX Claim 2; SEQ ID NO 573; 591pp; English.
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dlthp (ACC46080-ACC46749) and to their
 CC encoded proteins (Dlthp; ABR41136-ABR41812). The invention also relates
 CC to polynucleotide sequences at least 90% identical to the dlthp cDNA
 CC sequences of the invention; recombinant vectors; host cells and
 CC transgenic organisms comprising a dlthp nucleic acid sequence; the
 CC recombinant production of dlthp proteins; antibodies specific for dlthp
 CC proteins; microarrays comprising dlthp nucleic acid sequences; methods
 CC of detecting dlthp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a dlthp protein; and methods of
 CC assessing the toxicity of test compounds using a dlthp hybridisation
 CC probe. Dlthp nucleic acid sequences and dlthp proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. Dlthp
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dlthp nucleic acids are
 CC additionally useful in somatic or germ line gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a dlthp cDNA encoding a dlthp protein
 CC which is an organelle-associated protein.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcr_sequences.
 XX
 SQ Sequence 2213 BP; 422 A; 751 C; 633 G; 407 T; 0 other;
 Query Match 91.0%; Score 816.4; DB 25; Length 2213;
 Best Local Similarity 99.9%; Pred. No. 5.6e-159;
 Matches 817; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGACGGAACAGGCGCATCTCTTGGCAAAAGCTTGTGGCGAGCATCGCCCGCC 60
 Db 206 ATGACGGAACAGGCGCATCTCTTGGCAAAAGCTTGTGGCGAGCATCGCCCGCC 265
 Qy 61 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGGTCAACCTGCTGTGAGTCCAGCAC 120
 Db 266 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGGTCAACCTGCTGTGAGTCCAGCAC 325
 Qy 121 GCCAGCAACAGATCGCCCGCAGCAAGATCAAGAGGCGATGTGAGTCAATGTCGC 180
 Db 326 GCCAGCAACAGATCGCCCGCAGCAAGATCAAGAGGCGATGTGAGTCAATGTCGC 385
 Qy 181 ATCCCAAGAGAGCGGCGTGTCTCTTGTGAGGGGCAACCTTCCAAAGTCAATGTCG 240
 Db 386 ATCCCAAGAGAGCGGCGTGTCTCTTGTGAGGGGCAACCTTCCAAAGTCAATGTCG 445
 Qy 241 TACTTCCGACGCAACGCGCTCAACTTGGCTTCAAGAGATGAAGTCAAGAGATCTTCG 300
 Db 446 TACTTCCGACGCAACGCGCTCAACTTGGCTTCAAGAGATGAAGTCAAGAGATCTTCG 505

Oy	301	GGGGGGCGTGGACAAGCAACAGCGAGTTCGTGGAGAGTACTTTTGGGGCAACCTGGGCTCCGGG	360
Dd	506	GGGGGGCGTGGACAAGCAACAGCGAGTTCGTGGAGAGTACTTTTGGGGCAACCTGGGCTCCGGG	565
Oy	361	GGTGGGGGGGGGGGAGCTCCCTCTGTCGTGGTGTACACCGGTGGATTTTGGCGAGAACCGCG	420
Dd	566	GGTGGGGGGGGGGGAGCTCCCTCTGTCGTGGTGTACACCGGTGGATTTTGGCGAGAACCGCG	625
Oy	421	CTGGCAGCGCGACGTGGGAAAGTACGACAGACGCGCAGTTCGAGGCGCTGGGAGACTGC	480
Dd	626	CTGGCAGCGCGACGTGGGAAAGTACGACAGACGCGCAGTTCGAGGCGCTGGGAGACTGC	685
Oy	481	CTGTGTGAAGATCACCAAGTCCGACGGCATCCGGGGGCGCTGTACCAAGGCGCTTCAGTGTCTCC	540
Dd	686	CTGTGTGAAGATCACCAAGTCCGACGGCATCCGGGGGCGCTGTACCAAGGCGCTTCAGTGTCTCC	745
Oy	541	GTCACAGGGCATCATCATCTACCGGGGCGGCGCTACTTTCGGCGCTGTACGATACGGCCAAAGGGC	600
Dd	746	GTCACAGGGCATCATCATCTACCGGGGCGGCGCTACTTTCGGCGCTGTACGATACGGCCAAAGGGC	805
Oy	601	ATGCTACCCCGACCCCAAGAACACGCACATCGTGTGAGTGTATGATCCGACAGCCGTG	660
Dd	806	ATGCTACCCCGACCCCAAGAACACGCACATCGTGTGAGTGTATGATCCGACAGCCGTG	865
Oy	661	ACGGGCGTGGGGGGGGCGTGGTGTCTTACCCCTTTCGACACGGGTGGGGGGCGGCGCATGTATG	720
Dd	866	ACGGGCGTGGGGGGGGCGTGGTGTCTTACCCCTTTCGACACGGGTGGGGGGCGGCGCATGTATG	925
Oy	721	CAGTCCGGGGGGCCAAAGAGCTGTACATGTATACACGGGCAACGCTGCATCTTTGGAGAGAG	780
Dd	926	CAGTCCGGGGGGCCAAAGAGCTGTACATGTATACACGGGCAACGCTGCATCTTTGGAGAGAG	985
Oy	781	ATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGG	818
Dd	986	ATCTTCAGAGATGAGGGGGGCAAGGCGCTTCTTCAAGGG	1023
RESULT 8			
ABK83761			
ID ABK83761 standard; cDNA; 1116 BP.			
ABK83761;			
14-AUG-2002 (first entry)			
Human cDNA differentially expressed in granulocytic cells #312.			
Human; se; granulocytic cell; DNA chip; bacterial infection;			
viral infection; parasitic infection; protozoal infection;			
fungal infection; sterile inflammatory disease; psoriasis;			
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;			
cardiac reperfusion injury; renal reperfusion injury; ARDS;			
adult respiratory distress syndrome; inflammatory bowel disease;			
Crohn's disease; ulcerative colitis; periodontal disease;			
granulocyte activation; chronic inflammation; allergy.			
Homo sapiens.			
MO200228999-A2.			
11-APR-2002.			
03-OCT-2001; 2001MO-US10821.			
03-OCT-2000; 2000US-237189P.			
(GENE-) GENE LOGIC INC.			
Beazer-Barclay Y, Weltsman SM, Yamaga S, Vockley J;			
WPI; 2002-435328/46.			

PM Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 XX
 PS Claim 1, SEQ ID No 332, 114pp; English.

Claim 1; SEQ ID No 332; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g., psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIP0 at http://wipo.int/pub/published_pct_sequences.

SQ Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;

Query Match	Score	DB	Length
86.08;	771.2;	24;	1116;

Matches	786;	Conservative	0;	Mismatches	3;	Indels	3;	Gaps	1;
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QY 106 CTGCAGGTCACGACGCCAGCAAGCAGATGCCGCCGACACAAGCAGTACAAAGGCATCGTG 165

Db 1 CTGCAGGTCACGACGCCAGCAAGCAGATCGCCGCCGACCAAGCAGTACAAAGGCATCGTG 60

QY 166 GACTGCATTGTCCGCATCCCAAGAGAGCAGGCGTGTCTGTCCCTTCTGGAGGGCAACCTT 225

Db 61 GACTGCATTGTCGCCATCCCCAAGGAGCGAGGGGCTGTCCTTCTGGAGGGCAACCTT 120

QY 226 GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCCTCAAGGATAGTAC 285

Db 121 GCCACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCCTCAAGGATAAGTAC 180

286 AAGCAGTCTTCCTGGGGGGCGTGGACAAGCACACGCACTTCTGGAGGTACTTTGGGGC 345

Db 181 AAGCAGTCTTCTGGGGGGCTGGACAGACACGC---GTTCTGGAGGTACTTTGCGGGC 237

0x

346 AACAAAGGACGGTGAAGGACCAATCCTCCCGTCATTGCCTTTGTACTAACACCACA 405

[illegible][illegible][illegible]

OY	466	GGCCCTGGAGACACTGCTCTGGTGAAGATCAACAAAGTCCGAGGGCATCCGGGGCCTGTACCGAG	523
Db	358	GGCCTGGGAGACTGCTGGTGAAGATCAACAAAGTCCGAGGGCATCCGGGGCCTGTACCGAG	417
OY	526	GGCTTCAGTGTCTCCGTGCAGGGCATATCATCTACCGGGCGGCTTCTCGGCGGTAC	585
Db	418	GGCTTCAGTGTCTCCGTGCAGGGCATATCATCTACCGGGCGGCTTCTCGGCGGTAC	477
OY	586	GATACGGCCAAAGGGCATGCTCCCGACCCCAAGAAACAGCACATGCTGTAGCTGGATG	645
Db	478	GATACGGCCAAAGGGCATGCTCCCGACCCCAAGAAACAGCACATGCTGTAGCTGGATG	537
OY	646	ATCCGCGCAGACCGGTACCGCGCTGGCGCGCTGTGTCTTACCCTTTCACACAGGTGCGG	705
Db	538	ATCCGCGCAGACCGGTACCGCGCTGGCGCGCTGTGTCTTACCCTTTCACACAGGTGCGG	597
OY	706	CGGCGCAGATGATCATGCTCCGCGGGCGCAAAAGAGCTGACATCATGTACACGGGACCGTC	765
Db	598	CGGCGCAGATGATCATGCTCCGCGGGCGCAAAAGAGCTGACATCATGTACACGGGACCGTC	657
OY	766	GACTGTGTGGAGGAAGATCTTCCAGAGATGAGGGGGCAAGGGCCTTCTTCAAGGGTGCCTGG	825
Db	658	GACTGTGTGGAGGAAGATCTTCCAGAGATGAGGGGGCAAGGGCCTTCTTCAAGGGTGCCTGG	717
OY	826	TCCCAACGTCGTCGGGGGCGATGGGGGGCGCCTTCGTGTGTGCTGTACGACAGAGCTCAAG	885
Db	718	TCCCAACGTCGTCGGGGGCGATGGGGGGCGCCTTCGTGTGTGCTGTACGACAGAGCTCAAG	777
OY	886	AAGGTGATCTTAA	897
Db	778	AAGGTGATCTTAA	789
RESULT 9			
ID	ABN95598	ABN95598 standard; DNA; 1116 BP.	
XX	ABN95598;		
AC	13-AUG-2002	(first entry)	
DT	Gene #2096	used to diagnose liver cancer.	
XX	Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;		
KW	metastatic liver tumour; cytostatic; expression profile; disease state;		
KW	disease progression; drug toxicity; drug efficacy; drug metabolism.		
XX	Homo sapiens.		
OS	WO200229103-A2.		
XX	11-APR-2002.		
PD	02-OCT-2001; 2001WO-US30589.		
XX	02-OCT-2000; 2000US-237054P.		
PR	(GENE-) GENE LOGIC INC.		
XX	Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;		
PI	WPI: 2002-426119/45.		
DR	Diagnosing and detecting the progression of liver cancer,		
XX	hepatocellular carcinoma or metastatic liver tumor in a patient,		
PT	involves detecting the level of expression of two or more genes in a		
XX	liver tissue sample		
PS	Claim 1; SEQ ID NO 2096; 298bp; English.		
XX			
CC	The invention relates to a novel method for diagnosing and detecting the		
CC	progression of liver cancer, hepatocellular carcinoma or metastatic liver		

CC	tumour in a patient, and differentiating metastatic liver cancer from
CC	hepatocellular carcinoma in a patient, involving detecting the level of
CC	expression of two or more genes represented in ABN93503-ABN97435 in a
CC	tissue sample. The method of the invention has hepatotropic, and
CC	cytostatic activity. The method is useful for diagnosing and detecting
CC	the progression of liver cancer, hepatocellular carcinoma and metastatic
CC	liver carcinoma in a patient. The method is useful for identifying
CC	expression profiles which serve as useful diagnostic markers as well as
CC	markers that can be used to monitor disease states, disease progression,
CC	drug toxicity, drug efficacy and drug metabolism.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp://wipo.int/pub/published_pct_sequences.
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AAL48635
 ID AAL48635 standard; cDNA: 1225 BP.
 XX
 AC AAL48635;
 XX
 DT 11-Oct-2002 (first entry)
 XX
 DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 53.
 XX
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200255664-A2.
 XX
 PD 18-Jul-2002.
 XX
 PE 11-Jan-2002; 2002WO-US01048.
 XX
 PR 12-Jan-2001; 2001US-261226P.
 PR 12-Jan-2001; 2001US-261303P.
 PR 12-Jan-2001; 2001US-261304P.
 PR 12-Jan-2001; 2001US-261335P.
 PR 12-Jan-2001; 2001US-261336P.
 PR 12-Jan-2001; 2001US-261361P.
 PR 12-Jan-2001; 2001US-261456P.
 PR 12-Jan-2001; 2001US-261457P.
 PR 12-Jan-2001; 2001US-261458P.
 PR 12-Jan-2001; 2001US-261459P.
 PR 12-Jan-2001; 2001US-261461P.
 PR 12-Jan-2001; 2001US-261518P.
 PR 12-Jan-2001; 2001US-261531P.
 PR 12-Jan-2001; 2001US-261532P.
 PR 12-Jan-2001; 2001US-261589P.
 PR 12-Jan-2001; 2001US-261590P.
 PR 12-Jan-2001; 2001US-261694P.
 PR 12-Jan-2001; 2001US-261695P.
 PR 12-Jan-2001; 2001US-261697P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Seidel-Dugan C, Ferguson KC, Kidd T;
 XX
 DR WPI: 2002-599664/64.
 DR P-PSDB: AAO18516.
 XX
 PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent
 XX
 PS Disclosure; Page 159-160; 232pp; English.
 XX
 CC The present invention relates to a method of identifying a candidate
 CC insulin receptor (INR) signaling modulating agent, involving contacting
 CC an assay system comprising an insulin receptor signaling modifier (ISM)
 CC polypeptide or nucleic acid with a test agent, and detecting a test
 CC agent-biased activity of the assay system. The method is useful for
 CC identifying candidate INR signaling modulating agents. ISM genes may be
 CC used as drug targets for treatment of disorders related to INR signaling
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and
 CC polypeptides are useful for identifying and testing agents that modulate
 CC ISM function and for other applications related to the involvement of ISM
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM coding sequence described in the exemplification of the invention.
 XX
 SQ Sequence 1225 BP; 295 A; 300 C; 307 G; 323 T; 0 other;
 XX
 Query Match 66.5%; Score 596.2; DB 24; Length 1225;
 Best Local Similarity 79.0%; Pred. No. 1.2e-113;
 Matches 709; Conservative 0; Mismatches 188; Indels 0; Gaps 0

QY	1	ATACGAGCAACAGGCCATCTCCCTCTGCGCCAAAGACCTTTGGGCGGAGGACATCGCGCGCC	60
Db	69	ATBACAGATGCCCGCTGTGTCTTCCGCAAGACTTCTGTGGAGGTGGATGTGGCGACGCC	128
QY	61	ATCTCCAAAGCGCGGTGGCTTCGATCGAGGGGTCAAGCTGCTGTCAGGTCCAGCAC	120
Db	129	ATCTCCAAAGCGCGGTAGCGCCATCGAGGGGTCAAGCTGTGTCGACAGTGCACAT	188
QY	121	GCCAGCAACAGANTGCGCGCGCACAAAGCATACAAAGGCAATTCGTGACTGATTGTCCG	180
Db	189	GCCAGCAACAGATCACTGCAGATTAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT	248
QY	181	ATCCCAAGAGACAGGGCGTGTGCTGCTTTCGAGAGGGGCAACCTTGGCAAGTCAATCCG	240
Db	249	ATTCCCAAGAGACAGGAGATTCTGTCTTCTGTGGCGCGGTAACTCGGCCAATGTATACGA	308
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Db	309	TACTTCCCAACCCAGGCTCTTAACCTTCGCTTCAAGATTAATTAACAGCAAGATCTTCG	368
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Db	369	GGTGGTGTGAGACAAGAAACCCAGTTTGGCGCTCACTTGGAGGAATCTGCGCATCGGGT	428
QY	361	GGTGGCGCGCGCGCGACCTCTGCTGCTTGCCTGATACCGCGTGGATTTTGGCAGAACCGC	420
Db	429	GGTGGCGCGAGGGCCACATCTCCTGTGTGTTTGTGTACCTCTTGTATTTTGGCCGTAACCGT	488
QY	421	CTGGCAGCGGACGTGGGAAAGTCAAGCAGACAGCGCGAGTTCCGAGGCTTGGGAGACTGC	480
Db	489	CTAGCAGCTGATGTGGGTAAAGCTGTAGCTGAAAGGAATTCGAGGCGCTGGTGACTGC	548
QY	481	CTGGTGAAGATCAACCAAGTCCGACGGCATCCGGGGCTGTACAGGGCTTCAGTGTCTCC	540
Db	549	CTGGTTAAAGATCTACAAATCTGATGGGATTAAGGGCTGTACCAAGGCTTTAAGTGTCT	608
QY	541	GTCGAGGAGATCATCTATCCGGGCGGCTTACTTCGCGCTGTACGATACGGCCAAAGGC	600
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QY	781	ATCTTCAGAGATGAGGGGGCAAGGCCCTTTCGAAGGTTGGGTGCTCCACAGTCTCGG	840
Db	849	ATTGCTCTGATGATGAAGAGCAAAAGCTTTTTCGAAGGTTGATGATCCAAATGTTCTCGA	908
QY	841	GGCATGGGGGCGCCCTTCTGCTGTGTCTGTACGACGAGCTCAAGAAAGTATATA	897
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AAD00520 standard; cDNA: 897 BP.			
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29-AUG-2000 (first entry)			
Human adenine nucleotide translocator ANT2 cDNA.			
Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;			

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2003, 01:25:37 ; Search time 2414 Seconds

(without alignments)
9031.116 Million cell updates/sec

Title: US-09-811-094-3

Perfect score: 897
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

EST:*
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2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rnd:*
26: em_gss_pmg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.4	99.8	1355	11	BC013256 Homo sapi
2	895.4	99.8	1355	11	BC035469 Homo sapi
3	858.4	95.7	1201	13	BX419742 BX419742
4	850.8	94.8	1201	9	AL545701 AL545701

5	848	94.5	1201	9	AL534908
6	838.4	93.5	949	13	BQ932832
7	837.6	93.4	922	13	BQ226117
8	836.2	93.2	1201	9	AL540267
9	829.8	92.5	1201	9	AL539376
10	821.4	91.6	1201	9	AL557414
11	821	91.5	1201	9	AL514420
12	815.2	90.9	1071	12	BM554606
13	813.8	90.7	1014	13	BX375536
14	810.8	90.4	931	13	BQ933670
15	808.6	90.1	1201	13	BX423613
16	806.8	89.9	1201	9	AL542077
17	802.8	89.5	1093	9	AL550157
18	801	89.3	1201	13	BX375098
19	800	89.2	1030	12	BM476356
20	799.8	89.2	955	13	BQ677977
21	798.8	89.1	962	13	BX404094
22	798.2	89.0	973	13	BX447073
23	796	88.7	1201	9	AL568304
24	791.6	88.2	836	12	BI084258
25	790.6	88.1	951	13	BQ528404
26	789.8	88.0	1055	13	BX415427
27	789.6	88.0	1184	9	AL527028
28	788.6	87.9	1045	9	AL533037
29	788.6	87.9	1102	13	BX415022
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31	783.4	87.3	999	9	AL558781
32	780.6	87.0	915	13	BQ955091
33	778	86.7	1042	12	BM558078
34	777.6	86.7	920	13	BQ941868
35	777.4	86.7	969	10	BG759040
36	776.8	86.6	1010	12	BM603703
37	776	86.5	898	13	BQ849938
38	775.4	86.4	989	12	BM471365
39	773.2	86.2	944	9	AL555797
40	772.6	86.1	1017	12	BM608760
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45	765.4	85.3	932	13	BQ948479

ALIGNMENTS

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DEFINITION Homo sapiens, clone IMAGE:3865895, mRNA.
ACCESSION BC013256
VERSION BC013256.1 GI:15301544
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 1355)
JOURNAL Direct Submission
Submitted (27-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (TMCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villalondcm.tmc.edu.
 Villalón, D.R., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
 A.M., Hollway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 13 Row: e Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA g1: 3820534
 This clone has the following problem: no 5' EST match.

FEATURES

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 /organism="Homo sapiens"
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 /clone_image="3867130"
 /tissue_type="Eye, retinoblastoma"
 /clone_lib="NIH_MGC_67"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

BASE COUNT 283 a 417 c 404 g 251 t

ORIGIN

Query Match 99.8%; Score 895.4; DB 11; Length 1355;
 Best Local Similarity 99.9%; Pred. No. 8,4e-183;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 212 GCGACAGACAGGCGATCTCTTCGCAAGACTTTCGCGGAGAGCATCGCGCGCC 271
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 332 TACTTCCCATCTCAAGCCCTCACTTCGCTTCAAGAGTATGATCAAGAGATCTTCG 391
 301 GGGGGCGTGGACAGACAGGCGATCTTCGAGAGTATGATCAAGAGATCTTCG 360
 392 GGGGGCGTGGACAGACAGGCGATCTTCGAGAGTATGATCAAGAGATCTTCG 451
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 452 GGTGGGGCGTGGACAGACAGGCGATCTTCGAGAGTATGATCAAGAGATCTTCG 511
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 QY 781 ATCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 DB 872 ATCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
 QY 841 GCGATGGGGGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
 DB 932 GCGATGGGGGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 988

RESULT 2
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (nucleotide 1 to 1355)
 STRAUSBERG R.
 Direct Submission
 Submitted (31-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC) Cancer Genomics Office, National Cancer
 Institute, 31 Center drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT
 Email: gcraps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center:
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.M., Hale, S.M.,
 Lyon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 13 Row: f Column: 9
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA g1: 4503556
 This clone has the following problem: no 5' EST match.

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="3867130"
 /tissue_type="Eye, retinoblastoma"
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 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

BASE COUNT 283 a 417 c 404 g 251 t
 ORIGIN
 Query Match 99.8%; Score 895.4; DB 11; Length 1355;
 Best Local Similarity 99.9%; Pred. No. 8,4e-183;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGACGGAACAGCCATCTCTTCGCAAAAGCTTCTTGCGGAGGACATCCGCGCC 60
DB 92 ATGACGGAACAGCCATCTCTTCGCAAAAGCTTCTTGCGGAGGACATCCGCGCC 151
QY 61 ATCTCCAAAGAGCGGCTGCTCGATCGAGGGGTCGAACCTGCTGCTGAGGTCGACAC 120
DB 152 ATCTCCAAAGAGCGGCTGCTCGATCGAGGGGTCGAACCTGCTGCTGAGGTCGACAC 211
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DB 212 GCCAGCAAGCAGATGCGCCGCGACAAAGAGTACAAAGGCGATGTCATGTCATCCG 271
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DB 332 TACTTCCCAAGAGGAGGCTGCTGCTCTTCTGAGGGGCAACCTTCGAACGTCATTCG 391
QY 301 GGGGCGGTGAGACAGACAGCAGTCTGAGGATCTTTCGCGGCAACCTGCGCTCCG 360
DB 392 GGGGCGGTGAGACAGACAGCAGTCTGAGGATCTTTCGCGGCAACCTGCGCTCCG 451
QY 361 GGTGGGCGGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 452 GGTGGGCGGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 511
QY 421 CTGGGAGCGAGCTGGGAAAGTCAGGACAGAGCGGAGTCCGAGGCGCTGGGAGACTGC 480
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QY 481 CTGGTGAAGATACCAAGTCCGACGCGATCCGCGGCGCTTACAGGGCTTCAGTGTCTCC 540
DB 572 CTGGTGAAGATACCAAGTCCGACGCGATCCGCGGCGCTTACAGGGCTTCAGTGTCTCC 631
QY 541 GTGCAAGGATATATCTTACCGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 632 GTGCAAGGATATATCTTACCGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 691
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DB 692 ATGCTCCCGGACCCCAAGAACAGCAGCATGCTGAGTGTGATGATCGGCGAGACGCTG 751
QY 661 ACGGCGGTGGCGGCGGTGTCTTACCCCTTCGACAGCGGTGGGCGGCGCATGATGATG 720
DB 752 ACGGCGGTGGCGGCGGTGTCTTACCCCTTCGACAGCGGTGGGCGGCGCATGATGATG 811
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DB 872 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGATGCTGCTGCTGCTGCTGCTG 931
QY 841 GGCATGGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
DB 932 GGCATGGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988

RESULT 3
BX419742 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX419742 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF020YC16 5-PRIME, mRNA sequence.
ACCESSION BX419742
VERSION BX419742.1 GI:30642547
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r for
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF020B08Q1&cluster=10389.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF020B08Q1.

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/notes="Organ: Brain; Vector: pCMVSPORT.6; 1st strand cDNA
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vector. Library was not normalized."
BASE COUNT 245 a 365 c 354 g 210 t 27 others
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Best Local Similarity 97.8%; Pred. NO. 7.6e-175;
Matches 878; Conservative 11; Mismatches 7; Indels 2; Gaps 2;

QY 1 ATGACGGAACAGCCATCTCTTCGCAAAAGCTTCTTGCGGAGGACATCCGCGCC 60
DB 153 ATGACGGAACAGCCATCTCTTCGCAAAAGCTTCTTGCGGAGGACATCCGCGCC 211
QY 61 ATCTCCAAAGAGCGGCTGCTCGATCGAGGGGTCGAACCTGCTGCTGAGTCTGACAC 120
DB 212 ATCTCCAAAGAGCGGCTGCTCGATCGAGGGGTCGAACCTGCTGCTGAGTCTGACAC 271
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DB 272 GCCAGCAAGCAGATGCGCCGCGACAAAGAGTACAAAGGCGATGTCATGTCATCCG 331
QY 181 ATCCCAAGAGGAGGAGGCTGCTGCTCTTCTGAGGGGCAACCTTCGAACGTCATTCG 240
DB 332 ATCCCAAGAGGAGGAGGCTGCTGCTCTTCTGAGGGGCAACCTTCGAACGTCATTCG 391
QY 241 TACTTCCCAAGAGGAGGCTGCTGCTCTTCTGAGGGGCAACCTTCGAACGTCATTCG 300
DB 392 TACTTCCCAAGAGGAGGCTGCTGCTCTTCTGAGGGGCAACCTTCGAACGTCATTCG 451
QY 301 GGGGCGGTGAGACAGACAGCAGTCTGAGGATCTTTCGCGGCAACCTGCGCTCCG 360
DB 452 GGGGCGGTGAGACAGACAGCAGTCTGAGGATCTTTCGCGGCAACCTGCGCTCCG 511
QY 361 GGTGGGCGGCGGCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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QY 481 CTGGTGAAGATACCAAGTCCGACGCGATCCGCGGCGCTTACAGGGCTTCAGTGTCTCC 540
DB 632 CTGGTGAAGATACCAAGTCCGACGCGATCCGCGGCGCTTACAGGGCTTCAGTGTCTCC 691
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OY 541 GTGACAGGATCAT-CATCTACCGGGGGGCTTCTGCGGTGATAGATAGCCGCAAGG 599
 DB 692 GTGACAGGATCATCATCTACCGGGGGGCTTCTGCGGTGATAGATAGCCGCAAGG 751
 OY 600 CATGCTCCCGACCCCAAGACACACATGCTGATGATGATGATGATGATGATGATGAT 659
 DB 752 CATGCTCCCGACCCCAAGACACACATGCTGATGATGATGATGATGATGATGATGAT 811
 OY 660 GAGCG 719
 DB 812 GAGCG 871
 OY 720 GCACTCCG 779
 DB 872 GCACTCCG 931
 OY 780 GATCTTCAGATGAGGCG 839
 DB 932 GATCTTCAGATGAGGCG 991
 OY 840 GGGCG 897
 DB 992 GGGCG 1049

RESULT 4
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 LOCUS AL545701 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS001009YH03 5-PRIME, mRNA sequence.
 AL545701
 ACCESSION AL545701.2 GI:31267536
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12878183.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r for more information about this cluster, see
 http://www.genoscope.cns.fr/seq-clusters
 cgl-bin/cluster.cgi?seq=CS001009C020P1a1cluster-10389.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL: Corporation 1600
 http://fulllength.invitrogen.com/invitrogen
 Faraday Avenue Genoscope sequence ID : CS001009C020P1.
 Location/Qualifiers

FEATURES
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 Best Local Similarity 98.8%; Pred. No. 3,3e-173;
 Matches 878; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

OY 11 AGGCGATCTCTCTGCGCAAGACCTTCTTGCGGAGGATGCGCGCGCGCATCTCCAA 70
 DB 58 ATGCGATCTCTCTGCGCAAGACCTTCTTGCGGAGGATGCGCGCGCGCATCTCCAA 117
 OY 71 CGGCGCTGCGCTCCATGAGCGGCGTCAAGCTGCTGAGGTCACACCGACGACGAC 130
 DB 118 CGGCGCTGCGCTCCATGAGCGGCGTCAAGCTGCTGAGGTCACACCGACGACGAC 177
 OY 131 AGATCCCG 190
 DB 178 AGATCCCG 237
 OY 191 AGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
 DB 238 AGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
 OY 251 CTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
 DB 298 CTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
 OY 311 ACAAGACACGAGCTTCTGAGGATCTTCTGAGGATCTTCTGAGGATCTTCTGAGG 370
 DB 358 ACAAGACACGAGCTTCTGAGGATCTTCTGAGGATCTTCTGAGGATCTTCTGAGG 417
 OY 371 GCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
 DB 418 GCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
 OY 431 ACGTGGAAAGTCAGGACACAGCGCGCGAGTTCGAGGACCTGCGGAGACCTGCGTGA 490
 DB 478 ACGTGGAAAGTCAGGACACAGCGCGCGAGTTCGAGGACCTGCGGAGACCTGCGTGA 537
 OY 491 TCACCAAGTCGAGGACATCGGCGCGCTGCTGACCAAGGCTTCAAGTCTGCTGAGGGA 550
 DB 538 TCACCAAGTCGAGGACATCGGCGCGCTGCTGACCAAGGCTTCAAGTCTGCTGAGGGA 597
 OY 551 TCATCATCTACCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
 DB 598 TCATCATCTACCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
 OY 611 ACCCGAAGAACACGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670
 DB 658 ACCCGAAGAACACGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
 OY 671 CCGGCGTGTGCTTACCCCTTCGACACGCTGCGCGCGCGCGCATGATGATGATGATGAT 730
 DB 718 CCGGCGTGTGCTTACCCCTTCGACACGCTGCGCGCGCGCGCATGATGATGATGATGAT 777
 OY 731 GCAGAGAGCTGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790
 DB 778 GCAGAGAGCTGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
 OY 791 ATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 848
 DB 837 ATGAGGGGGGCAAGGCGCTTCTTCAAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 896
 OY 849 GGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 DB 897 GGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945

RESULT 5
 AL534908 1201 bp mRNA linear EST 12-MAY-2003
 LOCUS AL534908 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS00F007120 5-PRIME, mRNA sequence.
 AL534908
 ACCESSION AL534908.2 GI:30541165
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12798401.
 Contact--genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10389.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgl_bln/cluster.cgi?seq=CSODF007BE10QPlac1cluster-10389.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODF007BE10QPl.

FEATURES
 source
 1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODF007Y120"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 BASE COUNT 240 a 374 c 357 g 214 t 16 others
 ORIGIN

Query Match 94.5% Score 848; DB 9; Length 1201;
 Best Local Similarity 98.6%; Pred. No. 1.3e-172;
 Matches 885; Conservative 2; Mismatches 7; Indels 4; Gaps 3;
 1 ATGACGGAACAGAGCCATCTCTTCCGCAAAAGTCTTGGCGGAGCATCCGCGCCG 60
 161 ATGACGGAACAGAGCCATCTCTTCCGCAAAAGTCTTGGCGGAGCATCCGCGCCG 218
 61 ATCTCCAAAGAGCGCGTGGCTCCGATCGAGCGGGTCAGCTCTGCTGCAGGTCACAGC 120
 219 ATCTCCAAAGAGCGCGTGGCTCCGATCGAGCGGGTCAGCTCTGCTGCAGGTCACAGC 278
 121 GCCAGCAAGCAGATGGCGCGCGAGCAAGGATCAAGGGCATGTGAGTCACTGTCGCGC 180
 279 GCCAGCAAGCAGATGGCGCGCGAGCAAGGATCAAGGGCATGTGAGTCACTGTCGCGC 338
 181 ATCCCAAGAGCAGAGCGCGTGGCTCCGATCGAGCGGGTCAGCTCTGCTGCAGGTCACAGC 240
 339 ATCCCAAGAGCAGAGCGCGTGGCTCCGATCGAGCGGGTCAGCTCTGCTGCAGGTCACAGC 398
 241 TACTTCCCACTCAAGCCCTCAAGTTCGCTTCAAGGATTAAGTACAAAGCAGATCTTCTG 300
 399 TACTTCCCACTCAAGCCCTCAAGTTCGCTTCAAGGATTAAGTACAAAGCAGATCTTCTG 458
 301 GGGGGCGTGGAGCAAGCAGCAGTTCGAGTACTTGGCGGCAACTGGCCCTCCGCGC 360
 459 GGGGGCGTGGAGCAAGCAGCAGTTCGAGTACTTGGCGGCAACTGGCCCTCCGCGC 518
 361 GGTGGCGCGCGCGCACTCCCTGCTGCTGCTGTCACCCGCTGGATTTTCCAGAACCCGC 420
 519 GGTGGCGCGCGCGCACTCCCTGCTGCTGCTGTCACCCGCTGGATTTTCCAGAACCCGC 578
 421 CTGGAGCGGAGCTGGGAAAGTCAGGACAGAGCCGGAATTCGAGGCGCTGGAGACTGC 480
 579 CTGGAGCGGAGCTGGGAAAGTCAGGACAGAGCCGGAATTCGAGGCGCTGGAGACTGC 638
 481 CTGGTGAAGATCAACCAAGTCGAGCGGATCGGGGCGCTTACAGGCGCTTCAGTGTCTCC 540
 639 CTGGTGAAGATCAACCAAGTCGAGCGGATCGGGGCGCTTACAGGCGCTTCAGTGTCTCC 698

QY 541 GTGACGGGATCATCATCTACCGGGCGGCTTACTTGGCGGTGTACGATACGGCCAGAGGC 600
 DB 699 GTGACGGGATCATCATCTACCGGGCGGCTTACTTGGCGGTGTACGATACGGCCAGAGGC 758
 QY 601 ATGCTCCCGGACCCCAAGAACACGACATCTGTGTGAGTGTGATATGCGCGACCGTG 660
 DB 759 ATGCTCCCGGACCCCAAGAACACGACATCTGTGTGAGTGTGATATGCGCGACCGTG 818
 QY 661 ACGGCGGTGGCGGCGGTGTGCTTACCCCTTCGACAGCGTGGCGGCGCATGTGATG 720
 DB 819 ACGGCGGTGGCGGCGGTGTGCTTACCCCTTCGACAGCGTGGCGGCGCATGTGATG 878
 QY 721 CAGTCCGGCGGCAAGAGACTGACATGACAGGCGACCGTGCAGTGTGGAGAG 780
 DB 879 CAGTCCGGCGGCAAGAGACTGACATGACAGGCGA-CGTGAGCTGTGGAGAG 937
 QY 781 ATCTTCAGAGATGAGAGGGGCGCAAGGCTTCTTCAAGGGTGGCTCCACGCTCTCGCG 840
 DB 938 ATCTTCAGAGATGAGAGGGGCGCAAGGCTTCTTCAAGGGTGGCTCCACGCTCTCGCG 997
 QY 841 GGCAT-GGGGGCGGCGCTTCTGCTGCTGCTGTCAGACGAGCTCAAGAGGTGATCTAA 897
 DB 998 GGCATGGGGGCGGCGCTTCTGCTGCTGCTGTCAGACGAGCTCAAGAGGTGATCTAA 1055

RESULT 6 949 bp mRNA linear EST 21-AUG-2002
 BO932832
 AGENCOURT_8824122 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6459460
 LOCUS 5', mRNA sequence.
 DEFINITION BO932832.1 GI:22348215
 ACCESSION BO932832
 VERSION BO932832.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 949)
 AUTHORS NIH-MGC http://imgc.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2644 row: 3 column: 05
 High quality sequence stop: 674.

FEATURES
 source
 1. 949
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6459460"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_18"
 /note="Organ: lung; Vector: pORF7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 BASE COUNT 172 a 305 c 257 g 173 t 2 others
 ORIGIN

Query Match 93.5%; Score 838.4; DB 13; Length 949;
Best Local Similarity 97.8%; Pred. No. 1,5e-170;
Matches 870; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 1 ATGACGGAACAGGCGCATCTCTCTGCGCCAAAGACTTCTTGGCCCGAGAGCATCCCGCCGCC 60
DB 53 ATGACGGAACAGGCGCATCTCTCTGCGCCAAAGACTTCTTGGCCCGAGAGCATCCCGCCGCC 112
QY 61 ATTCGCAAGAGGCGCGTGGCTCCGATCGAGGGGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 113 ATTCGCAAGAGGCGCGTGGCTCCGATCGAGGGGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 172
QY 121 GCGCAGCAAGAGATGCGCGCGCGCAAGAGATGAGGAGGATGCTGTGATGATGATGATGATGATG 180
DB 173 GCGCAGCAAGAGATGCGCGCGCGCAAGAGATGAGGAGGATGCTGTGATGATGATGATGATGATG 232
QY 181 ATCCGCAAGAGAGAGGCGCGTGTCTCTTGTGAGGGGGCAACTTGTCCAAAGTCAATGTCG 240
DB 233 ATCCGCAAGAGAGAGGCGCGTGTCTCTTGTGAGGGGGCAACTTGTCCAAAGTCAATGTCG 292
QY 241 TACTTCCCACTCAAGCCTTCAATTCGCTTCAAGGATTAAGTAAAGATCTTCTCTG 300
DB 293 TACTTCCCACTCAAGCCTTCAATTCGCTTCAAGGATTAAGTAAAGATCTTCTCTG 352
QY 301 GGGGGCGGTGACAGACAGACAGATTTGAGAGTACTTTCGCGGCAACTGCGCTCCGCC 360
DB 353 GGGGGCGGTGACAGACAGACAGATTTGAGAGTACTTTCGCGGCAACTGCGCTCCGCC 412
QY 361 GGTGGCGCGCGCGACCTCTCTGCTGCTGTGATGACCGGTGAGATTTTCCAGAAACCCGC 420
DB 413 GGTGGCGCGCGCGACCTCTCTGCTGCTGTGATGACCGGTGAGATTTTCCAGAAACCCGC 472
QY 421 CTGGAGAGGAGAGGAGGAGATGACAGACAGAGGCGGAGTTCGAGAGCCTGGAGAGACTGC 480
DB 473 CTGGAGAGGAGAGGAGGAGATGACAGACAGAGGCGGAGTTCGAGAGCCTGGAGAGACTGC 532
QY 481 CTGGAGAGGAGATGACAGAGGAGATGACAGAGGAGGAGTTCGAGAGGAGTTCGAGAGGAG 540
DB 533 CTGGAGAGGAGATGACAGAGGAGATGACAGAGGAGGAGTTCGAGAGGAGTTCGAGAGGAG 592
QY 541 GTGAGAGGAGATGACATCTACCGGGGGGAGCTACTTGGGCGGTGATGATGATGATGATGATG 600
DB 593 GTGAGAGGAGATGACATCTACCGGGGGGAGCTACTTGGGCGGTGATGATGATGATGATGATG 652
QY 601 ATGCTCCCGGAGCGGAG 660
DB 653 ATGCTCCCGGAGCGGAG 712
QY 661 AGGCGCGGTGGCGCGGTGGTGTCTTACCGCTTTCGAGAGGAGTGGCGGCGGAGAGATGATG 720
DB 713 AGGCGCGGTGGCGCGGTGGTGTCTTACCGCTTTCGAGAGGAGTGGCGGCGGAGAGATGATG 772
QY 721 CAGTCCGCGGCGGAG 779
DB 773 CAGTCCGCGGCGGAG 832
QY 780 GATCTTCAGAGATGAGGGGGGAGAGGCTTCTTCAAGGGTGTGTGTGTGTGTGTGTGTGTGT 839
DB 833 GATCTTCAGAGATGAGGGGGGAGAGGCTTCTTCAAGGGTGTGTGTGTGTGTGTGTGTGTGT 892
QY 840 GGGCATGGGGGGCG-CCTTGT 888
DB 893 GGGCATGGGGGGCG-CCTTGT 942

RESULT 7
BO226117 922 bp mRNA linear EST 02-MAY-2002
LOCUS AGENCOURT.7576905 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6058842
DEFINITION 5' mRNA sequence.
ACCESSION BO226117.1 GI:20407526
VERSION
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bhs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13324 row: 1 column: 19
High quality sequence stop: 317.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6058842"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC_68"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally; primer: oligo dP;
Average insert size 1.8 kb. Library constructed by Life
Technologies".
BASE COUNT 184 a 296 c 280 g 162 t
ORIGIN

Query Match 93.4%; Score 837.6; DB 13; Length 922;
Best Local Similarity 96.7%; Pred. No. 2,2e-170;
Matches 866; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 1 ATGACGGAACAGGCGCATCTCTCTGCGCCAAAGACTTCTTGGCCCGAGAGCATCCCGCCGCC 60
DB 26 ATGACGGAACAGGCGCATCTCTCTGCGCCAAAGACTTCTTGGCCCGAGAGCATCCCGCCGCC 84
QY 61 ATCTCCAAAGAGGCGGTGCTCGATCGAGCGGCTCAAGCTGTCTCTCTCTCTCTCTCTCTCTCT 120
DB 85 ATCTCCAAAGAGGCGGTGCTCGATCGAGCGGCTCAAGCTGTCTCTCTCTCTCTCTCTCTCTCT 144
QY 121 GCGCAGCAAGAGATGCGCGCGCGAGACAGATGAGGAGGAGTGTGATGATGATGATGATGATG 180
DB 145 GCGCAGCAAGAGATGCGCGCGCGAGACAGATGAGGAGGAGTGTGATGATGATGATGATGATG 204
QY 181 ATCCGCAAGAGAGAGGCGGTGTCTCTTGTGAGGGGGCAACTTGTCCAAAGTCAATGTCG 240
DB 205 ATCCGCAAGAGAGAGGCGGTGTCTCTTGTGAGGGGGCAACTTGTCCAAAGTCAATGTCG 284
QY 241 TACTTCCCACTCAAGCCTTCAATTCGCTTCAAGGATTAAGTAAAGATCTTCTCTG 300
DB 265 TACTTCCCACTCAAGCCTTCAATTCGCTTCAAGGATTAAGTAAAGATCTTCTCTG 324
QY 301 GGGGGCGGTGACAGACAGACAGATTTGAGAGTACTTGGGAGAGAGAGAGAGAGAGAGAGAG 360
DB 325 GGGGGCGGTGACAGACAGACAGATTTGAGAGTACTTGGGAGAGAGAGAGAGAGAGAGAGAG 384
QY 361 GGTGGCGCGCGCGACCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 385 GGTGGCGCGCGCGACCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 444
QY 421 CTGGAGAGGAGATGACAGAGGAGATGACAGAGGAGGAGTTCGAGAGGAGTTCGAGAGGAG 480
DB 445 CTGGAGAGGAGATGACAGAGGAGATGACAGAGGAGGAGTTCGAGAGGAGTTCGAGAGGAG 504
QY 481 CTGGAGAGGATGACAGAGGAGATGACAGAGGAGGAGTTCGAGAGGAGTTCGAGAGGAG 540

Db 505 CTGTGAAGATGACCAAGTCGACGAGCATCGGGGCGCTTACCAAGCTTCAGTGTCTCC 564
 QY 541 GTGCAGGGCATCATCATCTACCGGGCGGCTACTTCCGGGTGACGATACGGCAAGGCG 600
 Db 565 ATGCAGGGCATCATCATCTACCGGGCGGCTACTTCCGGGTGACGATACGGCAAGGCG 624
 QY 601 ATGCTCCCGGACCCCAAGAACGACATCGTGTGATGATGATGATGATGATGATGATG 660
 Db 625 ATGCTCCCGGACCCCAAGAACGACATCGTGTGATGATGATGATGATGATGATGATG 684
 QY 661 ACAGCGGCGGCGGCGGTGTCTACCCCTTCGACAGCGGTGCGGGGCGCATGATGATG 720
 Db 685 ACAGCGGCGGCGGCGGTGTCTACCCCTTCGACAGCGGTGCGGGGCGCATGATGATG 744
 QY 721 CAGTCCGGGCGCAAGAGACTGACATGATGACAGCGGCGGTGCTGATGATGATGATG 780
 Db 745 CAGTCCGGGCGCAAGAGACTGACATGATGATGACAGCGGCGGTGCTGATGATGATG 804
 QY 781 ATCTTCAGAGATGAGAGGGGCAAGGCTTCTCAAGGGTGGCTGATGATGATGATGATG 840
 Db 805 ATCTTCAGAGATGAGAGGGGCAAGGCTTCTCAAGGGTGGCTGATGATGATGATGATG 864
 QY 841 GGCATGAGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 896
 Db 865 GGCATGAGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920

RESULT 8
 AL540267 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL540267 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF033YNO1 5-PRIME, mRNA sequence.

ACCESSION AL540267
 VERSION AL540267.2 GI:31264828
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12870254.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 10389.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF0332CG01Q1&cluster=10389.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF0332CG01Q1.

FEATURES
 source location/Qualifiers
 1..1201

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF033YNO1"
 /issue="FETAL BRAIN"
 /dev_stage="fetal"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

BASE COUNT 249 a 349 c 357 g 218 t 28 others
 ORIGIN

Query Match 93.2%; Score 836.2; DB 9; Length 1201;
 Best Local Similarity 99.2%; Pred. No. 4, 6e-170;
 Matches 860; Conservative 1; Mismatches 4; Indels 2; Gaps 2;
 QY 1 ATGACGAGACAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 Db 159 ATGACGAGAACAGGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 217
 QY 61 ATCTCCAGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 Db 218 ATCTCCAGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
 QY 121 GCCAGCAGCAGATGCGCGCGCGCGAGAACAGATGACAGGCGATGCTGATGCTGCGC 180
 Db 278 GCCAGCAGCAGATGCGCGCGCGCGAGAACAGATGACAGGCGATGCTGATGCTGCGC 337
 QY 181 ATCCCCAGAGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 338 ATCCCCAGAGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 397
 QY 241 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGATAGTACAGCAGATCTTCTG 300
 Db 398 TACTTCCCACTCAAGCCCTCAACTTGGCTTCAAGATAGTACAGCAGATCTTCTG 457
 QY 301 GGGGCGGTGAGACACAGCAGCAGATGCTGAGGATCTTGGCGGCAACTGGCTCCGCG 360
 Db 458 GGGGCGGTGAGACACAGCAGCAGATGCTGAGGATCTTGGCGGCAACTGGCTCCGCG 517
 QY 361 GGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 Db 518 GGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 577
 QY 421 CTGGCAGCGGAGCTGGGAAAGTACAGCAGAGCGGAGCTTCCGAGGCGTGGAGACTCG 480
 Db 578 CTGGCAGCGGAGCTGGGAAAGTACAGCAGAGCGGAGCTTCCGAGGCGTGGAGACTCG 637
 QY 481 CTGGTGAAGATCAACAGTCCGAGCGCATCCGGGCGCTTACAGGCGCTTCACTGCTCC 540
 Db 638 CTGGTGAAGATCAACAGTCCGAGCGCATCCGGGCGCTTACAGGCGCTTCACTGCTCC 697
 QY 541 GTGCAGGGCATCATCATCTACCGGGGCGGCTTCTGAGGATGATGATGATGATGATGATG 600
 Db 698 GTGCAGGGCATCATCATCTACCGGGGCGGCTTCTGAGGATGATGATGATGATGATGATG 757
 QY 601 ATGCTCCCGGACCCCAAGAACAGCAGATGCTGAGTGTGATGATGATGATGATGATG 660
 Db 758 ATGCTCCCGGACCCCAAGAACAGCAGATGCTGAGTGTGATGATGATGATGATGATG 817
 QY 661 ACAGCGGCGGCGGCGGTGTCTTACCCCTTGCACAGCGTGGCGGCGCATGATGATG 720
 Db 818 ACAGCGGCGGCGGCGGTGTCTTACCCCTTGCACAGCGTGGCGGCGCATGATGATG 877
 QY 721 CAGTCCGGGCGCAAGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATG 780
 Db 878 CAGTCCGGGCGCAAGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATG 937
 QY 781 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGGTGGCTGCTCAACGCTCTCGG 840
 Db 938 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGGTGGCTGCTCAACGCTCTCGG 997
 QY 841 GGCATGAGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
 Db 998 GGCATGAGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023

RESULT 9
 AL539376 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL539376 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF033YNO1 5-PRIME, mRNA sequence.
 ACCESSION AL539376
 VERSION AL539376.2 GI:31263944
 KEYWORDS EST.

BASE COUNT 239 a 358 c 348 g 222 t 34 others
 ORIGIN

Query Match 91.6%; Score 821.4; DB 9; Length 1201;
 Best Local Similarity 98.0%; Pred. No. 7.2e-167;
 Matches 877; Conservative 6; Mismatches 7; Indels 5; Gaps 5;

QY 1 ATGACGGAACAGCGCATCTCTTCCGCAAAAGACTTCTTGGCGGAGCATCGCCGCC 60
 DB 138 ATGACGGAACAGCGCATCTCTTCCGCAAAAGACTTCTTGGCGGAGCATCGCCGCC 196
 QY 61 ATCTCCAAAGAGCGCGTGGCTCCGATCGAGCGGCTGAAGCTGCTGTGACAGGCGAC 120
 DB 197 ATCTCCAAAGAGCGCGTGGCTCCGATCGAGCGGCTGAAGCTGCTGTGACAGGCGAC 256
 QY 121 GCCAGCAACAGATCGCCCGCCGCAAGAGATCAAGAGGATCGTGACATCTTCCG 180
 DB 257 GCCAGCAACAGATCGCCCGCCGCAAGAGGATCAAGAGGATCGTGACATCTTCCG 316
 QY 181 ATCCCAAGAGAGAGCGGCTGCTGTCTTGTGAGGCGCACTTGGCAAGTCATTCG 240
 DB 317 ATCCCAAGAGAGAGCGGCTGCTGTCTTGTGAGGCGCACTTGGCAAGTCATTCG 376
 QY 241 TACTTCCCACTCAAGCCCTCAACTCGCCTTCAAGGATTAAGTCAAGAGATCTTC 300
 DB 377 TACTTCCCACTCAAGCCCTCAACTCGCCTTCAAGGATTAAGTCAAGAGATCTTC 436
 QY 301 GGGGGCGGTGACAGCAGCAGCAGTCTGAGAGTACTTGGCGCAACCTGGCCTCG 360
 DB 437 GGGGGCGGTGACAGCAGCAGCAGTCTGAGAGTACTTGGCGCAACCTGGCCTCG 496
 QY 361 GGTGGCGCGCGCGCAGCTCTCTGCTTGTGTACCCGCTGGATTTTGGCAGACCC 420
 DB 497 GGTGGCGCGCGCGCAGCTCTCTGCTTGTGTGTACCCGCTGGATTTTGGCAGACCC 556
 QY 421 CTGGCAGCGAGCTGGGAAAGTCAAGGCAAGAGCGGAGTTCGAGGCGCGGAGACTG 480
 DB 557 CTGGCAGCGAGCTGGGAAAGTCAAGGCAAGAGCGGAGTTCGAGGCGCGGAGACTG 616
 QY 481 CTGGTGAAGATCAACAACTCCGAGCGCATCCGGGCTGTACAGGAGCTTCACTGTC 540
 DB 617 CTGGTGAAGATCAACAACTCCGAGCGCATCCGGGCTGTACAGGAGCTTCACTGTC 676
 QY 541 GTGACAGGCAATCACTACGCGGCGGCTTACTTGGCGGTGATCAATACGCGCAAG 600
 DB 677 GTGACAGGCAATCACTACGCGGCGGCTTACTTGGCGGTGATCAATACGCGCAAG 736
 QY 601 ATGCTCCCGAGCCGCAAGAACATGCAATCGTGTGAGTGAATGCGGCGAGACCTG 660
 DB 737 ATGCTCCCGAGCCGCAAGAACATGCAATCGTGTGAGTGAATGCGGCGAGACCTG 796
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 LOCUS AL514420 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
 DEFINITION CL0BB0102F01 5-PRIME, mRNA sequence.

ACCESSION AL514420
 VERSION AL514420.2 GI:30464305
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12777914.
 CONTACT Genoscope
 GENOSCOPE - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 EMAIL: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 LIBRARY was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10389.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CL0BB0102F01R1&cluster=10389.r. Contact :
 Feng Liang Email : fliang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CL0BB0102F01R1.
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 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: pCMVSPORT.6; 1st strand cDNA was primed
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 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT 233 a 346 c 370 g 219 t 33 others
 ORIGIN

Query Match 91.5%; Score 821; DB 9; Length 1201;
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 QY 361 GGTGGCGCGCGCGACCTCTCTGCTTGTGTACCCGCTGGATTTTGGCAAGACCCG 420
 DB 488 GGTGGCGCGCGCGACCTCTCTGCTTGTGTGTACCCGCTGGATTTTGGCAAGACCCG 547
 QY 421 CTGGCAGCGAGCTGGGAAAGTCAAGGCAAGAGCGGAGTTCGAGGCTGGGAGACTG 480

ACCESSION BX375536
 VERSION BX375536.1 GI:30456413
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1014)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r for more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC014BD120P1&cluster=10389.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DC014BD120P1.
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 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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 DB 518 GGTGGCGCGCGCGACCTCTCTGCTTGTACCCGCTGGATTTTGGCAGACCCGC 577
 QY 421 CTGGAGCGGAGCTGGGAAAGTCAAGCAGAGCGGAGTTCGAGGCGCTGGAGACTGC 480
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 ACCESSION BQ933670
 VERSION BQ933670.1 GI:22349053
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 931)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs@remail.nih.gov
 Tissue Procurement: DCTD/DPV/gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2605 row: 5 column: 05
 High quality sequence stop: 720.
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 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a


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QY 541 GTGCAGGGCATCATCATCTACCGGGGCGCTTCTCGGGGTGTACGATACGGCCAAAGGC 600
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Search completed: August 24, 2003, 03:33:47
 Job time : 2423 secs

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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (131)..(1027)
US-09-620-312D-687
Query Match 99.8%; Score 895.4; DB 4; Length 1212;
Best Local Similarity 99.9%; Pred. No. 2.7e-189;
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; Sequence 2, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleveland, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andrejev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelch, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-434-354-2

Query Match 66.3% Score 594.6; DB 4; Length 897;
Best Local Similarity 78.9%; Pred. No. 7, 6e-123;
Matches 708; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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RESULT 4

US-08-961-871-11

; Sequence 11, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: MacGregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1086
US-08-961-871-11

Query Match 65.9% Score 591.4; DB 3; Length 1259;
Best Local Similarity 78.7%; Pred. No. 4, 2e-122;
Matches 706; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

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DB 190 ATGGGGGATGAGGCTTGAAGCTTCTTAAAGACTTCTGAGAGGATGCTCCGCCGCC 249
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DB 250 GTCTCAAGAGGCGCGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGGTCAGC 309
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DB 490 GGGGCGCTGGACAGCAGCAGCTTCTGAGAGTACTTGGCGGCACTGCGCTCG 549
QY 361 GGTGCGCGCGCGCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 550 GGTGCGCGCGCGCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
QY 421 CTGGCAGCGGAGCTGGGAAAGTCAGGACAGCGCGAGTTCGAGGCTTGGAGACTGC 480
DB 610 CTGGCAGCGGAGCTGGGAAAGTCAGGACAGCGCGAGTTCGAGGCTTGGAGACTGC 669
QY 481 CTGTGAGAGTACACAGCAGCAGCTTCCGAGGCTTCTGAGAGGCTTCTGCTCC 540
DB 670 CTGACACAGAGTCTTCAAGTCCGAGGCTTCTGAGAGGCTTCTGCTCC 729
QY 541 GTGACGAGCATCATCATCTACCGGCGGCTTCTGAGGCTTCTGAGGCTTCTGAGG 600
DB 730 GTGACGAGCATCATCATCTACCGGCGGCTTCTGAGGCTTCTGAGGCTTCTGAGG 789
QY 601 ATGCTCCCGGACCGGCAAGACAGCGCATCTGAGGCTTCTGAGGCTTCTGAGG 660
DB 790 ATGCTCCCGGACCGGCAAGACAGCGCATCTGAGGCTTCTGAGGCTTCTGAGG 849
QY 661 AGCGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 850 AGCGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909
QY 721 CAGTCCGCGGCGCAAGAGGCTGATCATCTGACAGGCGCTGCTGCTGCTGCTG 780
DB 910 CAGTCCGCGGCGCAAGAGGCTGATCATCTGACAGGCGCTGCTGCTGCTGCTG 969
QY 781 ATCTTCAAGAGTCCGCGCGCAAGAGGCTTCTGAGAGGCTTCTGAGAGG 840
DB 970 ATCTTCAAGAGTCCGCGCGCAAGAGGCTTCTGAGAGGCTTCTGAGAGG 1029
QY 841 GGCATGGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
DB 1030 GGCATGGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1086

RESULT 5
US-08-961-871-9
Sequence 9, Application US/08961871
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11

1 CORRESPONDENCE ADDRESS:
ADDRESSER: Greenlee, Winer and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: 94..990
US-08-961-871-9

Query Match 65.6%; Score 588.2; DB 3; Length 1177;
Best Local Similarity 78.5%; Pred. No 2,1e-121;
Matches 704; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1 ATGACGAAACAGCCATCTCTCCGCAAGACTTCTTGGCCGAGGACATCCGCCGCC 60
DB 94 ATGGGGGATGAGGCTTGAAGCTTCTTAAAGACTTCTGAGGAGGCTCAAGCTTCTGAGG 153
QY 61 ATCTCAAGAGGCGCGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGGTCAGC 120
DB 154 GTCTCAAGAGGCGCGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGGTCAGC 213
QY 121 GCGACGAAAGAGTCCGCGCGCAAGAGTACAAAGGCACTGCGAGCTGCTCCGC 180
DB 214 GCGACGAAAGAGTCCGCGCGCAAGAGTACAAAGGCACTGCGAGCTGCTCCGC 273
QY 181 ATCCCAAGAGAGGCGCGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGG 240
DB 274 ATCCCAAGAGAGGCGCGCTCCGATCGAGCGGCTCAAGCTGCTGCGAGG 333
QY 241 TACTTCCGCACTCAAGCTTCCGCTTCAAGATGATACAGCAATCTTCTCG 300
DB 334 TACTTCCGCACTCAAGCTTCCGCTTCAAGATGATACAGCAATCTTCTCG 393
QY 301 GGGGCGCTGGACAGCAGCAGCTTCTGAGAGTACTTGGCGGCACTGCGCTCG 360
DB 394 GGGGCGCTGGACAGCAGCAGCTTCTGAGAGTACTTGGCGGCACTGCGCTCG 453
QY 361 GGTGCGCGCGCGCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 454 GGTGCGCGCGCGCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 513

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QY 421 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGACCGGAGTCCGAGGCTTGGGACACTGC 480
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 514 CTGGCGCGGACGTGGGAAAGTCTCCAGCGGAATTCATGCGGCGTGGCGACTGT 573
QY 481 CTGGTGAAGATCAACAAGTCCAGCGGACCTCGGAGGCTTACAGGGCTTCAAGTCTCC 540
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 574 CTCACCAAGATCTTCAAGTCGAGCGGCTGAAAGGGTCTTACAGGGCTTCAAGTCTCT 633
QY 541 GTGACAGGCGATCATCATCTACCGGGGCGCTTCTCGGCGGTGACATACGCGCAAGGCG 600
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 634 GTCCAGGCGCATCATCATCTACAGAGCTGCTTCTGAGTCTATGACACTGCGCAAGGGG 693
QY 601 ATGCTCCCCGACCCCAAGAACGACATCTGCTGATGATGATGATGATGATGATGATGAT 660
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 694 ATGCTGCCAGACCCCAAGAAATGTGCACATATCTGAGCTGATGATGATGATGATGATG 753
QY 661 ACAGCGCGTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 754 ACAGCGCGTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
QY 721 CAGTCCGGGCGCAAGAGACCTGACATGACACGCGGACCGTGCATGTTGGAGAGAG 780
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 814 CAGTCCGGGCGCAAGAGACCTGATATGATGATGATGATGATGATGATGATGATGATG 873
QY 781 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGGCTGCTCAAGCTCTGCGG 840
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 874 ATTCGAAAAGATGAAGAGACCAACGCTTCTTCAAGGGTGGCTGCTCAAGTACTGAGA 933
QY 841 GGCATGGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 934 GGCATGGGGTGGCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATG 990

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RESULT 6

US-09-434-354-1

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; Sequence 1, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigieri, Luciano G.
; APPLICANT: Velicelodi, Gennadi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-434-354-1

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Query Match 62.9%; Score 564.2; DB 4; Length 894;
Best Local Similarity 77.6%; Pred. No. 4e-116;
Matches 656; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

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QY 1 ATGACGAGACAGGCAATCTTCCGCAAGAGATCTTCCGAGGACATCGCGCGCC 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGGGATGATCAGCTTGGAGCTTCTTAAGAGATCTTCTGCGCGGCGGCGCTGCGC 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ATCTCCAAAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GTCTCCAAAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 GCGAGAGAGAGATGCGCGCGGAGAGAGATGATGATGATGATGATGATGATGATG 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 121 GCGAGAGAGAGATGCGCTGCTGAGAGAGATGATGATGATGATGATGATGATGATG 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 ATCCCAAGAGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATCCCAAGAGAGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 TACTTCCCAAGAGAGGCGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TACTTCCCAAGAGAGGCGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 GGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GGTGCGCGCGGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 GGGGGGCGGCGGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 CTGGCAGCGGAGCTGGGAAAGTCAAGGACAGACCGGAGTCCGAGGCGCTGGAGAGACTGC 480
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 TTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 CTGGTGAAGATCAACAAGTCCAGCGGACATCCGCGGCTTACAGGGGCTTCAAGTCTGCTC 540
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 ATATCAAGATCTTCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 537
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 GTGACAGGATCATCATCTACAGGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 GTGACAGGATCATCATCTATATAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 601 ATGCTCCCGAGACCCCAAGAACACGACATCTGCTGATGATGATGATGATGATGATGATG 660
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 ATGCTCCCGAGACCCCAAGAACGTCACATTTTGTGATGATGATGATGATGATGATGATG 657
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 661 ACAGCGCGTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 ACAGCGCGTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 721 CAGTCCGGGCGCAAGAGACCTGACATGATACAGCGGACCGTGCATGTTGGAGAGAG 780
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 CAGTCCGGGCGCAAGAGAGGCGGATATATGATACAGCGGAGAGTATGATGATGATG 777
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 781 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGGCTGCTGCTGCTGCTGCGG 840
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 778 ATTCGAAAAGAGACCAAGAGACCAAGGCGCTTCTTCAAGGGTGGCTGCTGCTGCTGCTG 837
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 841 GGCATGGGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 838 GGCATGGGGGCGGCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATG 894
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 7

US-09-016-434-622

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; Sequence 622, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 622:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVERUT04
CLONE: 2517151
US-09-016-434-622

Query Match
Best Local Similarity 99.3%; Score 186; DB 4; Length 289;
Matches 197; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGAGGAAAGGAGGATCTCTTCCGCAAGAGCTTCTTGGCCGAGAGCATCGCCGCC 60
DB 93 ATGAGGAAAGGAGGATCTCTTCCGCAAGAGCTTCTTGGCCGAGAGCATCGCCGCC 152
QY 61 ATCTCCAGAGCGGCGTGTCTCGATCGAGCGGGTCAAGCTCTGCTGACAGTCCAGC 120
DB 153 ATCTCCAGAGCGGCGTGTCTCGATCGAGCGGGTCAAGCTCTGCTGACAGTCCAGC 212
QY 121 GCCACAGAGAGATCGCGCGCGAGAGAGTACAGAGGAGGATGAGTGTCTCCG 180
DB 213 GCCACAGAGAGATCGCGCGCGAGAGAGTACAGAGGAGGATGAGTGTCTCCG 271
QY 181 ATCCCAAGAGAGAGG 198
DB 272 ATCCCAAGAGAGAGG 289

RESULT 8
US-08-518-878B-38
Sequence 38, Application US/08518878B
Patent No 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-518-878B-38

Query Match
Best Local Similarity 6.3%; Score 56.4; DB 1; Length 1255;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTCCGAGGCGCTGGAGACTGCTGTGAAGATCAACAAAGTCCGAGGATCCGGG 515
DB 141 CGAGTCCGAGGCGCTGGAGACTGCTGTGAAGATCAACAAAGTCCGAGGATCCGGG 200
QY 516 CCGTACAGAGGCTTCAAGTCTCCGTGAGAGGATCATCATCTACCGGGGCGCTACT 575
DB 201 CCGTACAGAGGCTTCAAGTCTCCGTGAGAGGATCATCATCTACCGGGGCGCTACT 260
QY 576 CGGCGGTACAGTACAGGCGGATCGTCCCGGACCCCAAGAGAGAGCATCGG 635
DB 261 CGGCGGTACAGTACAGGCGGATCGTCCCGGACCCCAAGAGAGAGCATCGG 320
QY 636 GAGCTGATGATCGCGCAGACCGCTGACGCGCGCGCTGCTCTACCCCTTCA 695
DB 321 GAGCTGATGATCGCGCAGACCGCTGACGCGCGCGCTGCTCTACCCCTTCA 380
QY 696 CAGGTCGCGCGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
DB 381 GAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 440
QY 756 GGGCAGCCCTGACTTGTGAGAGATCTTGAAGATGAGAGGAGGAGGAGGAGGAG 815
DB 441 AAGCAGCCCTGACTTGTGAGAGATCTTGAAGATGAGAGGAGGAGGAGGAGGAG 500
QY 816 GGGTGTGCTGCTCAAGCTCTGCGGGGAGATGAGGAGGAGGAGGAGGAGGAGG 875
DB 501 AAGCAGCCCTGACTTGTGAGAGATCTTGAAGATGAGAGGAGGAGGAGGAGGAG 560
QY 876 CGAGCTCAAGAGG 889
DB 561 TGACCTCATCAAGG 574

RESULT 9
US-08-294-522B-38
Sequence 38, Application US/08294522B
Patent No 5741666
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-522B-38

Query Match 6.3%; Score 56.4; DB 1; Length 1255;
Best Local Similarity 45.6%; Pred. No. 0.00074;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTTCGAGGCGCTGGAGACTGCTGTGAAGATCACCAAGTCCGAGGGATCGGGG 515
DB 141 CCAATACCGCGGTGATGATGGGACCACTTGTGACCATGTGCTGAGGGGCCCGGAAAG 200
QY 516 CCGTACCAAGGCTTCAGTCTCCGTGCGAGGCGCATCATCTACCGGGCGCTACTT 575
DB 201 CCTCTCAATAGGGCTGTGGTGGCGGCTGAGCGCCAAATAGAGTTGGCTGTGTCCGAT 260
QY 576 CGGCGGTACGATACGCGCAAGGGCATGCTCCCGACCCCAAGACAGCAGCATCTGCT 635
DB 261 CGGCGGTATGATTCGTCAAAACAGTTCTACACCAAGGGCTGTGACATGCGCAGCATTTG 320
QY 636 GAGCTGATGATGCGGCGAGACCGTGCAGGCGCGGCGGCGGTGCTCTCAACCTTCGA 695
DB 321 GAGCGCGCTCTTACGAGGAGCAGCAGCAGGTGCGCTGTGCTGTGGCCAGCCGAC 380
QY 696 CAGCGTGGCGGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
DB 381 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 440
QY 756 GGGCAGCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
DB 441 AAGCAGCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
QY 816 GGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 875
DB 501 AGGAGCTCTCCCAATGTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 560
QY 876 CGAGCTCAAGAAAG 889
DB 561 TGACCTCATCAAGG 574

RESULT 10
US-08-470-868A-38
Sequence 38, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITL OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-38

Query Match 6.3%; Score 56.4; DB 2; Length 1255;
Best Local Similarity 45.6%; Pred. No. 0.00074;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTTCGAGGCGCTGGAGACTGCTGTGAAGATCACCAAGTCCGAGGGATCGGGG 515
DB 141 CCAATACCGCGGTGATGATGGGACCACTTGTGACCATGTGCTGAGGGGCCCGGAAAG 200
QY 516 CCGTACCAAGGCTTCAGTCTCCGTGCGAGGCGCATCATCTACCGGGCGCTACTT 575
DB 201 CCTCTCAATAGGGCTGTGGTGGCGGCTGAGCGCCAAATAGAGTTGGCTGTGTCCGAT 260
QY 576 CGGCGGTACGATACGCGCAAGGGCATGCTCCCGACCCCAAGACAGCAGCATCTGCT 635
DB 261 CGGCGGTATGATTCGTCAAAACAGTTCTACACCAAGGGCTGTGACATGCGCAGCATTTG 320
QY 636 GAGCTGATGATGCGGCGAGACCGTGCAGGCGCGGCGGCGGTGCTCTCAACCTTCGA 695
DB 321 GAGCGCGCTCTTACGAGGAGCAGCAGCAGGTGCGCTGTGCTGTGGCCAGCCGAC 380
QY 696 CAGCGTGGCGGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
DB 381 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 440
QY 756 GGGCAGCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
DB 441 AAGCAGCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
QY 816 GGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 875
DB 501 AGGAGCTCTCCCAATGTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 560
QY 876 CGAGCTCAAGAAAG 889
DB 561 TGACCTCATCAAGG 574

RESULT 11
US-08-807-861A-38
Sequence 38, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITL OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York

Mon Aug 25 09:31:43 2003

us-09-811-094-3.rn1

Page 8

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 51A
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-807-861A-38

Query Match 6.3% Score 56.4; DB 2; Length 1596;
Best Local Similarity 45.6%; Pred. No. 0.00078;
Matches 198; Mismatches 236; Indels 0; Gaps 0;
DB 456 CGAGTCCGAGGCGCTGGAGAGCTCCCTGGTGAAGTACACCAAGTCCGAGCGCATCCGGGG 515
DB 483 CCAAGTACCGGGGTGTGATGGGACCAATCTGTACATGTCGTACTAGAGGGCCCGGAG 542
DB 516 CCGTACCGAGGGCTTCAAGTCTCCGTCCAGGGCATCATCTTACCGGGCGCTACTT 575
DB 543 CCTGTACAAATGGGCTGTGGCCGGCTGACGCGCAATAGCTTGGCTTGTCTGCGCAT 602
DB 576 CGGCGTGTACATAGGCGCAAGGCGATCTCCCGACCCCAAGACACGACATGCTGT 635
DB 603 CGGCTGTATGATCTGTCAAAAGTCTTACCAAGGCTTGACATGACATGCGCATTTGG 662
DB 636 GAGCTGATATGAGCGACAGACGTCGCGCCGTGGCGGCTGTCTTCTTACCGCTTGA 695
DB 663 GAGCGGCTCTCTGACAGGCGACCAAGTGTGCTGGTGTGGTGGTGGCCACCGAC 722
DB 696 CAGGCTGGGGGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
DB 723 GAGTGTGTAAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 782
DB 756 GGGACCGTGTGATGTTGAGAGAAATCTTCAAGATGAGAGGGGGGCAAGGCTTCTTAA 815
DB 783 AAGCACCGTAAATGCTTACAAAGACATTTGCGGAGAGAGAGGTTCCGGGGGCTCTGAA 842
DB 816 GGGTGGCTGTCCACAGCTCTCGGGGAGCATGGGGGGCGCTTGTGTCTGTCTGTCTGACA 875
DB 843 AGGAGACCTTCCTCAATGTTGTGTGAATGCAATGTGTCACTGTGAGACTGTGATGCTTA 902
DB 876 CGAGCTCAAGAGG 889
DB 903 TGACCTCATCAAGG 916

RESULT 12
US-09-210-681-38
Sequence 38, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
Applicant: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Pennine & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-210-681-38

Query Match 6.3% Score 56.4; DB 3; Length 1596;
Best Local Similarity 45.6%; Pred. No. 0.00078;
Matches 198; Mismatches 236; Indels 0; Gaps 0;
DB 456 CGAGTCCGAGGCGCTGGAGAGCTCCCTGGTGAAGTACACCAAGTCCGAGCGCATCCGGGG 515
DB 483 CCAAGTACCGGGGTGTGATGGGACCAATCTGTACATGTCGTACTAGAGGGCCCGGAG 542
DB 516 CCGTACCGAGGGCTTCAAGTCTCCGTCCAGGGCATCATCTTACCGGGCGCTACTT 575
DB 543 CCTGTACAAATGGGCTGTGGCCGGCTGACGCGCAATAGCTTGGCTTGTCTGCGCAT 602
DB 576 CGGCGTGTACATAGGCGCAAGGCGATCTCCCGACCCCAAGACACGACATGCTGT 635
DB 603 CGGCTGTATGATCTGTCAAAAGTCTTACCAAGGCTTGACATGACATGCGCATTTGG 662
DB 636 GAGCTGATATGAGCGACAGACGTCGCGCCGTGGCGGCTGTCTTCTTACCGCTTGA 695
DB 663 GAGCGGCTCTCTGACAGGCGACCAAGTGTGCTGGTGTGGTGGTGGCCACCGAC 722
DB 696 CAGGCTGGGGGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755

Db 723 GGATGTTGTAAGTCCATTCACAGTCACGGCCGGGCTGAGGTTGGAGATACCA 782
QY 756 GGGCACCCCTGCAGCTTTGGAGAGATCTTCAGAGATGAGGGGGCAAGCCCTCTTCAA 815
Db 783 AAGCACCCGTCATGCTTACAGACCATTCGCCGAGAGAAAGGTTCCGGGGCCCTCTGAA 842
QY 816 GGGTGGTGTCCACAGTCCTGCTGGGGCATGGGGGGCCCTCTGCTGTGCTGTGACCA 875
Db 843 AAGGACCTCTCCCAATGTTGCTGTATATGCCATTTGTCAACTGTGCTGAGCTGTGACCTA 902
QY 876 CGAGCTCAAGAAG 889
Db 903 TGACCTCATCAAG 916

RESULT 13
US-08-946-719A-38
Sequence 38, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-946-719A-38

Query Match 5.3%; Score 56.4; DB 3; Length 1596;
Best Local Similarity 45.6%; Pred. No. 0.00078;
Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTTCGAGCGCTGGAGATCGCTGTGAAGATCACCAAGTCGAGCGGCGGGG 515
Db 483 CCAAGTACCGCGGTGTATGGGACCATTTGTGACCATGTGTGCTACTGAGGGCCCGGAAAG 542

QY 516 CCTGTACAGGCGCTTCACTGTCTCCGTGCAGGGCATCATCATACCGGGCGGCTACTT 575
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QY 576 GGGCGTGTACATAGGCGCAAGGCGATGCTCCCGCAACCCCAAGAAACGCAATGTGT 635
Db 603 CGGCGTATATGTTCTGTCAAAAGTTCTTACACAAAGGCGCTGTGAGCATGCGAGATTGG 662
QY 636 GAGCTGATGATCGCGACAGCGGTGAGCGCCGTGGCGCGGCGTGTCTTACCCTTGA 695
Db 663 GAGCGGCTCTTACAGAGGAGCAGCAGAGGTGCTGCTGTGTGCTGTGCGCCAGCCAC 722
QY 696 CAGGTGCGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
Db 723 GGATGTTGTAAGTCCATTCACAGTCACGGCCGGGCTGAGGTTGGAGATACCA 782
QY 756 GGGCACCCCTGCAGCTTTGGAGAGATCTTCAGAGATGAGGGGGCAAGCCCTCTTCAA 815
Db 783 AAGCACCCGTCATGCTTACAGACCATTCGCCGAGAGAAAGGTTCCGGGGCCCTCTGAA 842
QY 816 GGGTGGTGTCCACAGTCCTGCTGGGGCATGGGGGGCCCTCTGCTGTGCTGTGACCA 875
Db 843 AAGGACCTCTCCCAATGTTGCTGTATATGCCATTTGTCAACTGTGCTGAGCTGTGACCTA 902
QY 876 CGAGCTCAAGAAG 889
Db 903 TGACCTCATCAAG 916

RESULT 14
US-09-547-983-38
Sequence 38, Application US/09547983
Patent No. 6518402
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,983
FILING DATE: 12-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1596 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 US-09-547-983-38

Query Match 6.3%; Score 56.4; DB 4; Length 1596;
 Best Local Similarity 45.6%; Pred. No. 0.00078;
 Matches 198; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 456 CGAGTTCGAGGCGCTGGAGACTGCTGCTGAGATCACCAGTCCGACGCGCATCCGAGG 515
 DB 483 CCAGTACCGCGGTGTATGGGACCATCTGACCATGTGCTGATGAGGAGGCGCCCGAG 542
 QY 516 CCTGTACGAGGCTTCACTGTCTCCGTGACGAGGATCATCATCTACCGGAGGCTTACTT 575
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 QY 576 CGGCGTGTACGATACGCGCAGAGGCGATGCTCCCGACCCAGACACGACATCTGTGT 635
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 DB 723 GATGTGTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 782
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 QY 816 GGGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
 DB 843 AAGGAGCTCTCCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
 QY 876 CGAGCTCAGAGG 889
 DB 903 TGACCTCAGAGG 916

RESULT 15
 US-09-142-565-1
 Sequence 1, Application US/09142565A
 Patent No. 6187560
 GENERAL INFORMATION:
 APPLICANT: Lee James Bealey
 APPLICANT: Kelly Paine
 APPLICANT: Robert James
 FILE OF INVENTION: MODEL COMPOUNDS
 FILE REFERENCE: GH-30002
 CURRENT APPLICATION NUMBER: US/09/142,565A
 CURRENT FILING DATE: 1998-06-30
 EARLIER FILING DATE: 1997-03-05
 EARLIER APPLICATION NUMBER: 9705614.7
 EARLIER FILING DATE: 1997-03-18
 EARLIER APPLICATION NUMBER: 97305305.1
 NUMBER OF SEQ ID NOS: 6
 SOURCE: Passed for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 1192
 TYPE: DNA
 ORGANISM: HOMO SAPIEN
 US-09-142-565-1

Query Match 6.0%; Score 54.2; DB 3; Length 1192;

Best Local Similarity 48.5%; Pred. No. 0.0022;
 Matches 217; Conservative 0; Mismatches 216; Indels 12; Gaps 2;
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 QY 635 TGTGCTGATGATGCGGACAGC-----GTGAGCGCGTGGCGCGGTGTGCT 685
 DB 548 CTACCGGATTTTGGCGGCTGACACACAGAGCCATGCGGCTGCTGTGCTGCTGCT 607
 QY 686 ACCCTGTGACGCGTGGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGAT 745
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 QY 746 TGTGTACGAGGCGACCGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 805
 DB 668 GAAATATACGCGGACCTATGAGCGCTTACAGAACATGCGCAGAGGAGAGGATCAGG 727
 QY 806 CTTTGTGAGGCTGCGCGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 865
 DB 728 GCTGTGTGAGAGGATCTTGTGCGCAATCATGAGGATGATGATGATGATGATGATGAT 892
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 Job time : 77 secs

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: August 24, 2003, 03:33:53 ; Search time 252 Seconds
(without alignments)
8002.392 Million cell updates/sec

Title: US-09-811-094-3

Perfect score: 897
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	897	100.0	897	9	US-09-810-644-3
3	897	100.0	897	10	US-09-185-904A-3
4	895.4	99.8	1212	14	US-10-037-270-687
5	873.4	97.4	2392	13	US-10-044-090-152
6	771.2	86.0	1116	10	US-09-969-708-213
7	771.2	86.0	1116	10	US-09-880-107-2096
8	771.2	86.0	1116	14	US-10-171-581-48
9	596.2	66.5	1196	10	US-09-917-800A-1327
10	594.6	66.3	897	9	US-09-811-094-2
11	594.6	66.3	897	9	US-09-810-644-2
12	594.6	66.3	897	10	US-09-185-904A-2
13	581.8	64.9	1711	14	US-10-198-846-13437
14	564.2	62.9	894	9	US-09-811-094-1
15	564.2	62.9	894	9	US-09-810-644-1
16	564.2	62.9	894	10	US-09-185-904A-1

C	17	482.4	53.8	2706	14	US-10-103-313-611	Sequence 611, App
	18	429	47.8	468	11	US-09-918-995-26014	Sequence 26014, A
	19	412	45.9	493	11	US-09-918-995-9153	Sequence 9153, A
	20	394	43.9	720	9	US-09-910-943-105	Sequence 105, App
	21	392.4	43.7	410	11	US-09-918-995-16539	Sequence 16539, A
	22	363.2	40.5	460	11	US-09-918-995-4700	Sequence 4700, App
	23	334	37.2	420	11	US-09-918-995-5524	Sequence 5524, App
	24	318.6	35.5	434	10	US-09-960-352-12424	Sequence 12424, A
	25	318.4	35.5	413	11	US-09-918-995-35706	Sequence 35706, A
	26	317	35.3	409	9	US-09-925-301-617	Sequence 617, App
	27	306	34.1	424	11	US-09-918-995-17465	Sequence 17465, A
	28	302.8	33.8	501	11	US-09-833-790-161	Sequence 161, App
	29	299	33.3	390	11	US-09-918-995-5492	Sequence 5492, App
	30	298.4	33.3	416	11	US-09-918-995-37003	Sequence 37003, A
	31	296	33.0	487	9	US-09-864-761-1488	Sequence 1488, App
	32	286.4	31.9	402	11	US-09-918-995-37381	Sequence 37381, A
	33	282.2	31.5	483	11	US-09-918-995-1495	Sequence 1495, App
	34	280	31.2	858	14	US-10-198-846-9464	Sequence 9464, App
	35	278.8	31.1	408	10	US-09-960-352-14278	Sequence 14278, A
	36	275	30.7	324	10	US-09-960-352-14747	Sequence 14747, A
	37	274	30.5	513	11	US-09-918-995-37948	Sequence 37948, A
	38	266.4	29.7	417	11	US-09-918-995-5864	Sequence 5864, App
	39	266.4	29.7	464	9	US-09-864-761-1408	Sequence 1408, App
	40	265.8	29.6	474	11	US-09-918-995-6148	Sequence 6148, App
	41	264.6	29.5	485	11	US-09-918-995-8792	Sequence 8792, App
	42	264.2	29.5	484	11	US-09-918-995-6070	Sequence 6070, App
	43	242.6	27.0	443	9	US-09-864-761-3148	Sequence 3148, App
	44	240.4	26.8	1536	9	US-09-734-569-169	Sequence 169, App
	45	226	25.2	927	14	US-10-128-714-2338	Sequence 2338, App

ALIGNMENTS

US-09-811-094-3
Sequence 3, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleverger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
US-09-811-094-3
Query Match 100.0%; Score 897; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 5.3e-227;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGGAACAGCCATCTCTTCCGCAAGACTTTTGGCCGAGGCATCGCCGCC 60
DB 1 ATGACGGAACAGCCATCTCTTCCGCAAGACTTTTGGCCGAGGCATCGCCGCC 60
QY 61 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGCTCAACTGCTGAGAGTCCAGCAC 120
DB 61 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGCTCAACTGCTGAGAGTCCAGCAC 120

US-09-185-904A-3
 ; Sequence 3, Application US/09185904A
 ; Patent No. US2002017185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Cleveland, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185,904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 897
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-185-904A-3

Query Match 100.0%; Score 897; DB 10; Length 897;
 Best Local Similarity 100.0%; Pred. No. 5.3e-227;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACGAGAACGCGCATCTCTCCGCAAAAGCTTCTGGCGGAGCATCCGCGCGC 60
 1 ATGACGAGAACGCGCATCTCTCCGCAAAAGCTTCTGGCGGAGCATCCGCGCGC 60
 61 ATCTCCAGACGCGCGCTGCTCCGATCGAGCGGCTCAAGCTCTGCTGAGGTCCAGC 120
 61 ATCTCCAGACGCGCGCTGCTCCGATCGAGCGGCTCAAGCTCTGCTGAGGTCCAGC 120
 121 GCCAGCAAGCAGATGCGCGCGAGCAAGCAAGTCAAGAGGCGATCTGAGTGTCCGC 180
 121 GCCAGCAAGCAGATGCGCGCGAGCAAGCAAGTCAAGAGGCGATCTGAGTGTCCGC 180
 181 ATCCCAAGAGCAGGCGGCTGCTCTCTGAGAGGCGCAAGCTTGCAGAGCTCATTCGC 240
 181 ATCCCAAGAGCAGGCGGCTGCTCTCTGAGAGGCGCAAGCTTGCAGAGCTCATTCGC 240
 241 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGAGTAAATAGACAGAGATCTCTCG 300
 241 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGAGTAAATAGACAGAGATCTCTCG 300
 301 GGGGCGGTGAGACACACAGCAGTCTGAGAGTACTTGGCGGCAACCTGACCTCCGCG 360
 301 GGGGCGGTGAGACACACAGCAGTCTGAGAGTACTTGGCGGCAACCTGACCTCCGCG 360
 361 GGTGGGCGGCGGCGGCGCTCTGCTCTGCTGATCCGCTGATTTTCCGAAACCCGC 420
 361 GGTGGGCGGCGGCGGCGCTCTGCTCTGCTGATCCGCTGATTTTCCGAAACCCGC 420
 421 CTGGAGCGGAGAGTGGGAAGTCAAGCAGAGAGCGAGTTCGAGAGCTTGAGAGCTGC 480
 421 CTGGAGCGGAGAGTGGGAAGTCAAGCAGAGAGCGAGTTCGAGAGCTTGAGAGCTGC 480
 481 CTGTGAGAGATACCAAGTCCGAGCGCATCCGCGGCTGTACCAAGGCTTCAAGTGTCTCC 540
 481 CTGTGAGAGATACCAAGTCCGAGCGCATCCGCGGCTGTACCAAGGCTTCAAGTGTCTCC 540
 541 GTGACGGGCGATCATCTAAGCGGCGGCTCTACTTCCGCGGTAGAGTACAGGCGCAAGGCG 600
 541 GTGACGGGCGATCATCTAAGCGGCGGCTCTACTTCCGCGGTAGAGTACAGGCGCAAGGCG 600
 601 ATGCTCCCGACCCCAAGAACAGCAGATCTGTGTAGTGTAGTATCCGAGACCGTG 660
 601 ATGCTCCCGACCCCAAGAACAGCAGATCTGTGTAGTGTAGTATCCGAGACCGTG 660

661 ACGCCGTGGCGCGGCTGCTCTAACCCTTCCAGACAGGTGCGCGCGCATGATGATG 720
 661 ACGCCGTGGCGCGGCTGCTCTAACCCTTCCAGACAGGTGCGCGCGCATGATGATG 720
 721 CAGTCCGGGCGCAAGGAGCTGACATGATGACAGGGGACCGTGCAGCTGTGGAGAG 780
 721 CAGTCCGGGCGCAAGGAGCTGACATGATGACAGGGGACCGTGCAGCTGTGGAGAG 780
 781 ATCTTCAGAGATGAGGGGCGCAAGGCTTCTCAAGGGTGTGCTGCAACGCTCCGCGG 840
 781 ATCTTCAGAGATGAGGGGCGCAAGGCTTCTCAAGGGTGTGCTGCAACGCTCCGCGG 840
 841 GGCATGGGGGCGCGCTTGTGCTGCTGTACGACGAGCTCAAGAGGTGATCTAA 897
 841 GGCATGGGGGCGCGCTTGTGCTGCTGTACGACGAGCTCAAGAGGTGATCTAA 897

RESULT 4

US-10-037-270-687
 ; Sequence 687, Application US/10037270
 ; Publication No. US20030104529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Xue, Aldong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhou, Pian
 ; APPLICANT: Ma, Yundong
 ; APPLICANT: Wang, Dairui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Tillinghast, John
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 784C1P2B
 ; CURRENT APPLICATION NUMBER: US/10/037,270
 ; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; NUMBER OF SEQ ID NOS: 1104
 ; SOFTWARE: PL_Fl_genes Version 1.0
 ; SEQ ID NO 687
 ; LENGTH: 1212
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (131)..(1027)
 ; US-10-037-270-687

Query Match 99.8%; Score 895.4; DB 14; Length 1212;
 Best Local Similarity 99.9%; Pred. No. 1.4e-226;
 Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGACGAGAACGCGCATCTCTCCGCAAAAGCTTCTGGCGGAGCATCCGCGCGC 60
 131 ATGACGAGAACGCGCATCTCTCCGCAAAAGCTTCTGGCGGAGCATCCGCGCGC 190
 61 ATCTCCAGACGCGCGTGCCTCGATCGAGCGGCTCAAGCTCTGCTGAGGTCCAGCAC 120
 191 ATCTCCAGACGCGCGTGCCTCGATCGAGCGGCTCAAGCTCTGCTGAGGTCCAGCAC 250
 121 GCCAGCAAGCAGATGCGCGCGAGCAAGCAGTCAAGAGGCGATCTGTGACTGTGTCGC 180

251 GCCAGCAGCAGATGCGCCGACACAGTACAAAGGCGATGCTGACTGATTTGCCG 310
181 ATCCCCAAGAGCAGGCGCTGCTGCTTCTGAGAGGGGCAACCTTGCCAACTGATTCG 240
311 ATCCCCAAGAGAGGCGGCTGCTGCTGCTGAGAGGGGCAACCTTGCCAACTGATTCG 370
241 TACTTCCCACTCAAGCCCTCACTGAGCTTCAAGGATTAAGTACAAAGATCTTCCTG 300
371 TACTTCCCACTCAAGCCCTCACTGAGCTTCAAGGATTAAGTACAAAGATCTTCCTG 430
301 GGGGGGCTGAGACACACACAGAGTTCGAGAGTTCGAGGAGCACTTGCGGCAACCTGCGGCG 360
431 GGGGGGCTGAGACACACACAGAGTTCGAGAGTTCGAGGAGCACTTGCGGCAACCTGCGGCG 490
361 GGGGGGCTGAGACACACACAGAGTTCGAGAGTTCGAGGAGCACTTGCGGCAACCTGCGGCG 420
491 GGGGGGCTGAGACACACACAGAGTTCGAGAGTTCGAGGAGCACTTGCGGCAACCTGCGGCG 550
421 CTGGCAGCGAGCTGAGGAAAGTCAAGCCACAGCGAGTTCGAGGAGCACTTGCGGCAACCTGCG 480
551 CTGGCAGCGAGCTGAGGAAAGTCAAGCCACAGCGAGTTCGAGGAGCACTTGCGGCAACCTGCG 610
481 CTGGTGAAGATCCACAGTCCGAGCGCATCCGCGGCGCTTACCAGGCTTCAGTGTCTCC 540
611 CTGGTGAAGATCCACAGTCCGAGCGCATCCGCGGCGCTTACCAGGCTTCAGTGTCTCC 670
541 GTGCGAGGCTATCTATCTACCGGGGCGCTTACTTGGCGGTGATGATACGAGCCAAAGGCG 600
671 GTGCGAGGCTATCTATCTACCGGGGCGCTTACTTGGCGGTGATGATACGAGCCAAAGGCG 730
DB 601 ATGCTCCCCACCCCAAGAACACGACATGCTGTGAGTGTGATGATGATGATGATGATGATGATG 660
QY 721 ATGCTCCCCACCCCAAGAACACGACATGCTGTGAGTGTGATGATGATGATGATGATGATGATG 790
DB 661 ACGGCGCTGGCGCGCTGTGTCTTACCCCTTTCGACACAGGCTGCGGCGGCGCATGATGATG 720
QY 791 ACGGCGCTGGCGCGCTGTGTCTTACCCCTTTCGACACAGGCTGCGGCGGCGCATGATGATG 850
DB 721 CAGTCCCGGCGCAAGAGACTGACATGATGACAGCGGCGACCTGCACTGTTGGAGAGAG 780
QY 851 CAGTCCCGGCGCAAGAGACTGACATGATGACAGCGGCGACCTGCACTGTTGGAGAGAG 910
DB 781 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGATGATGATGATGATGATGATG 840
QY 911 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGATGATGATGATGATGATGATG 970
DB 841 GGCATGGGGGGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
QY 971 GGCATGGGGGGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
DB
RESULT 5
US-10-044-090-152
; Sequence 152, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 152
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
; LOCATION: 1131, 1929
; OTHER INFORMATION: a, t, c, g, or other

US-10-044-090-152
Query Match 97.4%; Score 873.4; DB 13; Length 2592;
Best Local Similarity 99.7%; Pred. No. 9,9e-221;
Matches 896; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
1 ATGAGGAAGAGGCGCATCTCTTGGCAAGAGTCTTGGCGGAGGAGCAT -CGCGCGCG 59
207 ATGAGGAAGAGGCGCATCTCTTGGCAAGAGTCTTGGCGGAGGAGCAT -CGCGCGCG 266
DB 267 CATCTCAAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
QY 60 CATCTCAAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
DB 267 CATCTCAAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
QY 119 ACGCGAGAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
DB 327 ACGCGAGAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
QY 179 GATCCCCAAGAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
DB 387 GATCCCCAAGAGAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
QY 239 GCTACTTCCCACTCAAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
DB 447 GCTACTTCCCACTCAAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
QY 239 GCTACTTCCCACTCAAGAGGCGCGGCTCGATCGAGCGGGGTCAGCTCTGCTGAGGTCACAG 326
DB 507 TGGGGGCGCTGGAGACAGACAGAGTTCGAGAGTTCGAGAGTTCGAGAGTTCGAGAGTTCGAGAGTTCG 358
QY 359 GCGGTCGCGCGCGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418
DB 567 GCGGTCGCGCGCGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
QY 419 GCGTGGCAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCGAGAGTTCGAGAGTTCGAGAGTTCG 478
DB 627 GCGTGGCAGCGAGCTGGGAAAGTCAAGGACAGAGCGGAGTTCGAGAGTTCGAGAGTTCGAGAGTTCG 686
QY 479 GCGTGGTGAAGATCCAGAGTCCGACGCGGCGGCGGCTTACCAGGCTTCAGTGTCT 538
DB 687 GCGTGGTGAAGATCCAGAGTCCGACGCGGCGGCGGCTTACCAGGCTTCAGTGTCT 746
QY 539 CCGTGGAGGCGCATCTATCTTACCGGCGGCGGCTTACCAGGCTTCAGTGTCT 598
DB 747 CCGTGGAGGCGCATCTATCTTACCGGCGGCGGCTTACCAGGCTTCAGTGTCT 806
QY 599 GCATGCTCCCGACCCCAAGAACACGACATGCTGTGAGTGTGATGATGATGATGATGATGATGATG 658
DB 807 GCATGCTCCCGACCCCAAGAACACGACATGCTGTGAGTGTGATGATGATGATGATGATGATGATG 866
QY 659 TGAAGGCGCGTGGCGCGGCTGTGTCTTACCCCTTTCGACACAGGCTGCGGCGGCGCATGATGATG 718
DB 867 TGAAGGCGCGTGGCGCGGCTGTGTCTTACCCCTTTCGACACAGGCTGCGGCGGCGCATGATGATG 926
QY 719 TGAAGTCCGGGGGCAAGAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
DB 927 TGAAGTCCGGGGGCAAGAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 986
QY 779 AGATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGATGATGATGATGATGATGATG 838
DB 987 AGATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGCCTGATGATGATGATGATGATGATG 1046
QY 839 GGGGCGATGGGGGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
DB 1047 GGGGCGATGGGGGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1105

RESULT 6
US-09-969-708-213
; Sequence 213, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena

QY 646 ATCCGAGACCGTGAAGGCGCTGGCCGCTGGTGTCTACCTTCCTGACACGGTGGCG 705
| | | | |
DB 538 ATCCGAGACCGTGAAGGCGCTGGCCGCTGGTGTCTACCTTCCTGACACGGTGGCG 597
| | | | |
QY 706 CGGCGCATGATGATGAGTCTCCGGGCGCAAGAGACCTGACATCATGTACACGGGCAACGCTC 765
| | | | |
DB 598 CGGCGCATGATGATGAGTCTCCGGGCGCAAGAGACCTGACATCATGTACACGGGCAACGCTC 657
| | | | |
QY 766 GACTGTGGAGGAAGATCTTCAAGATGAGGGGGGCAAGGCGCTTCTCAAGGGTGGCTGG 825
| | | | |
DB 658 GACTGTGGAGGAAGATCTTCAAGATGAGGGGGGCAAGGCGCTTCTCAAGGGTGGCTGG 717
| | | | |
QY 826 TCCAAAGCTCTCGGGGGGCAATGGGGGCGCTTCTGCTGTCTCTTACGACGAGCTCAAG 885
| | | | |
DB 718 TCCAAAGCTCTCGGGGGGCAATGGGGGCGCTTCTGCTGTCTCTTACGACGAGCTCAAG 777
| | | | |
QY 886 AAGGTGATCTAA 897
| | | | |
DB 778 AAGGTGATCTAA 789
| | | | |

RESULT 8
US-10-171-581-48
; Sequence 48, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao Mao
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,914
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 366
; SEQ ID NO 48
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: J03592
; DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-48

Query Match 86.08; Score 771.2; DB 14; Length 1116;
Best Local Similarity 99.28; Pred. No. 7.9e-194;
Matches 786; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
QY 106 CTGAGATTCAGACGCGCAGCAAGATGCGCGCGACAGAGATACAAAGGGCATCGTG 165
| | | | |
DB 1 CTGAGATTCAGACGCGCAGCAAGATGCGCGCGACAGAGATACAAAGGGCATCGTG 60
| | | | |
QY 166 GACTGATTTGCGCATTCGCCAAGAGAGAGGCGTGTCTCTTCTGAGGGGCAACCTT 225
| | | | |
DB 61 GACTGATTTGCGCATTCGCCAAGAGAGAGGCGTGTCTCTTCTGAGGGGCAACCTT 120
| | | | |
QY 226 GCCAAGCTCATTCGCTACTTCCCACTCAAGCCCTCAACTCCCTCAAGGATTAAGTAC 285
| | | | |
DB 121 GCCAAGCTCATTCGCTACTTCCCACTCAAGCCCTCAACTCCCTCAAGGATTAAGTAC 180
| | | | |
QY 286 AAGCAGATCTTCTGGGGGGGCGTGACAAAGCAGAGATTTGAGAGTACTTTCGGGGC 345
| | | | |
DB 181 AAGCAGATCTTCTGGGGGGGCGTGACAAAGCAGAGATTTGAGAGTACTTTCGGGGC 237
| | | | |
QY 346 AACCTGGCTCGGGGGGCGTGACGGGCGGCGGCGCTCTCTCTGCTGCTGTAACCGCTGAT 405
| | | | |
DB 238 AACCTGGCTCGGGGGGCGTGACGGGCGGCGGCGCTCTCTCTGCTGCTGTAACCGCTGAT 297
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QY 406 TTTGCCAAGAACCGGCTTGGCAGCGAGATGCTGAGAAATGACAGCAGAGCGGAGTTCGGA 465
| | | | |
DB 298 TTTGCCAAGAACCGGCTTGGCAGCGAGATGCTGAGAAATGACAGCAGAGCGGAGTTCGGA 357
| | | | |

QY 466 GGCCTGGAGACTGCTGTGTGATGATACCAAGTCCAGAGCATCCGGGGCTGTACAG 525
| | | | |
DB 358 GGCCTGGAGACTGCTGTGTGATGATACCAAGTCCAGAGCATCCGGGGCTGTACAG 417
| | | | |
QY 526 GGCCTGAGTGTCTCCGTCAGAGGATCATCATCTACCGGGGCGCTTACTTGGGGTATC 585
| | | | |
DB 418 GGCCTGAGTGTCTCCGTCAGAGGATCATCATCTACCGGGGCGCTTACTTGGGGTATC 477
| | | | |
QY 586 GATACGGCCAAAGGAGATGCTCCCGACCCCAAGAACCCATCATCTGTAAGTGGATG 645
| | | | |
DB 478 GATACGGCCAAAGGAGATGCTCCCGACCCCAAGAACCCATCATCTGTAAGTGGATG 537
| | | | |
QY 646 ATCCGAGACCGTGAAGGCGCTGGCCGCTGGTGTCTACCTTCCTGACACGGTGGCG 705
| | | | |
DB 538 ATCCGAGACCGTGAAGGCGCTGGCCGCTGGTGTCTACCTTCCTGACACGGTGGCG 597
| | | | |
QY 706 CGGCGCATGATGATGAGTCTCCGGGCGCAAGAGACCTGACATCATGTACACGGGCAACGCTC 765
| | | | |
DB 598 CGGCGCATGATGATGAGTCTCCGGGCGCAAGAGACCTGACATCATGTACACGGGCAACGCTC 657
| | | | |
QY 826 TCCAAAGCTCTCGGGGGGCAATGGGGGCGCTTCTGCTGTCTCTTACGACGAGCTCAAG 885
| | | | |
DB 718 TCCAAAGCTCTCGGGGGGCAATGGGGGCGCTTCTGCTGTCTCTTACGACGAGCTCAAG 777
| | | | |
QY 886 AAGGTGATCTAA 897
| | | | |
DB 778 AAGGTGATCTAA 789
| | | | |

RESULT 9
US-09-917-800A-1327
; Sequence 1327, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1327
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Rattus norvegicus

Query Match	Best Local Similarity	Matches	Score	DB %	Length	Indels	Gaps
66.3%;	78.9%;	0;	594.6;	9;	897;	189;	0;
Conservative		Mismatches					
<p>GENERAL INFORMATION:</p> <p>APPLICANT: Anderson, Christen M.</p> <p>APPLICANT: Davis, Robert E.</p> <p>APPLICANT: Clevenger, William</p> <p>APPLICANT: Wiley, Sandra Eileen</p> <p>APPLICANT: Miller, Scott W.</p> <p>APPLICANT: Szabo, Thomas R.</p> <p>APPLICANT: Ghosh, Soumitra S.</p> <p>APPLICANT: Moos, Walter H.</p> <p>APPLICANT: Pel, Yezhong</p> <p>TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),</p> <p>FILE REFERENCE: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR</p> <p>CURRENT FILING DATE: 2001-03-14</p> <p>NUMBER OF SEQ ID NOS: 37</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 2</p> <p>LENGTH: 897</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapien</p> <p>US-09-811-094-2</p>							
1	ATGACGGAAAGCGGCATCTCTGCGCAAAGACTTCTGGCGGAGGCATGCGCGCGCC	60					
1	ATGACAGATGCGCGCATGTGCTCTGCGCAAAGACTTCTGGCGGAGGCATGCGCGCGCC	60					
61	ATCTCCAAAGACGGCGCGCTCCGATCGAGCGCGGTCAAGCTCTGCTGAGGTCCAGCAC	120					
61	ATCTCCAAAGACGGCGCGGTAGCGCCCATCGAGCGGGGTCAACTGCTGCTGAGGTCCAGCAT	120					
121	GCCAGCAAGCAGATGCGCGCGCGACAGCATCAAGGGCATGCTGATGTCATTTGCGCG	180					
121	GCCAGCAAGCAGATGCTGACATCAAGCATCAAAAGCATTAATGACTGCGGTGCGCGT	180					
181	ATGCCAAGAGGACGAGGGGCTGTCCTTCTGAGAGGGGCACACTTGGCAAAGCATTTGCG	240					
181	ATGCCAAGAGGACGAGAGTTGTCCTTCTGAGAGGGGCACACTTGGCAAAGCATTTGCG	240					
241	TACTTCCCACTCAAGCCCTCAACTGCGCTTCAAGGATTAAGTACAAAGCATCTTCTG	300					
241	TACTTCCCACTCAAGCGCTTCAACTGCGCTTCAAGGATTAAGTACAAAGCATCTTCTG	300					
301	GGGGGCGTGACACGACGAGTTCTGGAGGTACTTTGCGGGCAACTGGCGTCCGCG	360					
301	GGTGGTGAGACAAAGAACCCAGTTTGGCGCTACTTTGCAGAGGAATCGGCATCGGGT	360					
361	GSTGGGCGCGGCGGACCTCCCTTCGCTCGGTACACCGCGTGGATTTTGCAGAACCGCG	420					
361	GSTGGGCGCGGCGGACCTCCCTTCGCTCGGTACACCGCGTGGATTTTGCAGAACCGCG	420					
421	CTGGCAGCGAGAGTGGGAAGTCAAGACAGACGCGGATTTCCGAGCGCTGGAGACTGC	480					
421	CTGGCAGCGAGAGTGGGAAGTCAAGACAGACGCGGATTTCCGAGCGCTGGAGACTGC	480					
481	CTGTGAAGATCACCAAGTCCGAGCGCATCCGCGGCGCTGTACCAAGGCTTCAAGTCTCC	540					
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541	GTGCGAGGCGATCATATCTACCGCGCGCGCTTACTTGGCGGTGATCATACGCGCAAGGGC	600					
541	GTGCGAGGCGATCATATCTACCGCGCGCGCTTACTTGGCGGTGATCATACGCGCAAGGGC	600					
601	ATGCGCCCCGACCCCAAGAACGACATCGAGGTGATGATTCGCGAGACGCTG	660					
601	ATGCGCCCCGACCCCAAGAACGACATCGAGGTGATGATTCGCGAGACGCTG	660					
661	ACGGCGGTGGCGGCGGTGTCTTACCCCTTCGACACGCTGCGCGCGCATGATGATG	720					

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:01:32 : Search time 83 Seconds
(without alignments)
569,886 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGGIAA.....LRGMCARVLYLDELKRYI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	21	AAV71033
2	1543	100.0	298	22	AAAM39641
3	1543	100.0	298	23	AAU01200
4	1543	100.0	298	23	AAU10380
5	1543	100.0	323	22	AAAM41427
6	1463	94.8	298	23	AAO18516
7	1454	94.2	298	21	AAV71032
8	1454	94.2	298	21	AAU01199
9	1454	94.2	298	23	AAU10379

10	1418	91.9	429	24	ABR41715
11	1412	91.5	298	19	AAW61169
12	1406	91.1	293	22	ABU53219
13	1385.5	89.8	297	21	AAV71031
14	1385.5	89.8	297	22	AAU01198
15	1385.5	89.8	297	23	AAU10378
16	1367.5	88.6	325	22	ABG15423
17	1288	83.5	263	23	ABG27056
18	1254.5	81.3	299	22	ABG66082
19	1254.5	81.3	299	22	ABG66082
20	1137.5	73.7	307	22	ABG58380
21	1119	72.5	315	22	ABU53218
22	1119	72.5	315	23	ABE21175
23	1044	67.7	228	23	ABP74106
24	981	63.6	222	23	ABP74106
25	879.5	57.0	298	22	ABG18922
26	788.5	51.1	301	23	ABP73357
27	763	49.4	484	22	ABG15422
28	749.5	48.6	484	22	ABG27055
29	743	48.2	379	24	AAU00106
30	742.5	48.1	346	21	AAG37261
31	742.5	48.1	346	21	AAG37261
32	742.5	48.1	346	21	AAG37261
33	742.5	48.1	346	21	AAG37264
34	742.5	48.1	346	21	AAG38460
35	742.5	48.1	363	21	AAG36576
36	742.5	48.1	363	21	AAG37260
37	742.5	48.1	363	21	AAG37263
38	742.5	48.1	363	21	AAG38459
39	742.5	48.1	381	21	AAG36575
40	742.5	48.1	381	21	AAG37259
41	742.5	48.1	381	21	AAG37262
42	742.5	48.1	381	21	AAG38458
43	742.5	48.1	992	21	AAG38672
44	742.5	48.1	1009	21	AAG38671
45	742.5	48.1	1027	21	AAG38670

ALIGNMENTS

RESULT 1	
AAV71033	AAV71033 standard; Protein; 298 AA.
XX	XX
AC	AAV71033;
XX	XX
DT	29-AUG-2000 (first entry)
XX	XX
DE	Human adenine nucleotide translocator ANT3.
XX	XX
KW	Human: adenine nucleotide translocator: ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotrophic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparkinson; cerebroprotective; therapeutic; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	XX
OS	Homo sapiens.
XX	XX
PN	W0200026370-A2.
PD	11-MAY-2000.
XX	XX
PF	03-NOV-1999; 99WO-US25883.
XX	XX
PR	03-NOV-1998; 98US-0185904.
XX	08-SEP-1999; 99US-0393441.
XX	XX

PA (MITO-) MITOKOR.
 XX Anderson-CM, ~~David~~ RE, Clewenger W, Wiley SE, Miller SW, Szabo TR;
 PI Gosh SS;
 XX WPI: 2000-365619/31.
 DR N-PSDB: AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Claim 46; Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, hyperproliferative
 CC encephalopathy, lactic acidosis and stroke (MEAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX
 SO Sequence 298 AA:
 XX
 Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVYKLLQVOHASKQIADKQYKGYDCIYR 60
 DB 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVYKLLQVOHASKQIADKQYKGYDCIYR 60
 QY 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLAGS 120
 DB 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
 QY 181 VOGIITIRAAVFGVYDTAKGMLDPRKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
 DB 181 VOGIITIRAAVFGVYDTAKGMLDPRKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
 QY 241 OSGRKADIMYTGTVDCMKRIFRDEGKAFPKGAMSVNLGMCAGAVLVLYDELKVI 298
 DB 241 OSGRKADIMYTGTVDCMKRIFRDEGKAFPKGAMSVNLGMCAGAVLVLYDELKVI 298

RESULT 2
 ID AA39641 standard; Protein; 298 AA.
 XX
 AC AA39641;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 KM Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KM Chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KM Leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HXSE-) HXSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AA158797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA38642-AA42213), with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 SO Sequence 298 AA:
 XX
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVYKLLQVOHASKQIADKQYKGYDCIYR 60
 DB 1 MTEQATISFAKDFLAGGIAAISTKTAAPIERVYKLLQVOHASKQIADKQYKGYDCIYR 60
 QY 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLAGS 120
 DB 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFAFTRILADVGKSGTEREFGGLGDCLVKRTKSDGIRGLYQGFVS 180
 QY 181 VOGIITIRAAVFGVYDTAKGMLDPRKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240
 DB 181 VOGIITIRAAVFGVYDTAKGMLDPRKNTHTIVSWMIAQTVTAAGVVSYPFDVRRMM 240

OY 241 OSGRKADIMYGTGDCWKRIFRDEGKAFKFGANSNVLKRGGAFLVLYDELKVI 298
 DB 241 OSGRKADIMYGTGDCWKRIFRDEGKAFKFGANSNVLKRGGAFLVLYDELKVI 298

RESULT 3
 AAU01200
 ID AAU01200 standard; Protein; 298 AA.
 XX AAU01200;
 AC AAU01200;
 DB 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS WO200132876-A2.
 PN 10-MAY-2001.
 PD 03-NOV-2000; 2000MO-US30535.
 PE 03-NOV-1999; 99US-0434354.
 PR (MITO-) MITOKOR.
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Filiger LG;
 PI Velleblehl G, Davis RE;
 XX MPI: 2001-291054/30.
 DR N-PSDB; AAS05903.
 DR New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX Disclosure; Fig 2; 186bp; English.
 PS The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 SO Sequence 298 AA;
 OY Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MPEQATSPKADFLAGGIAAAISTAVAPIERVKLLQVHASKQIAADKQYGIYDCIYR 60
 |||

DB 1 MPEQATSPKADFLAGGIAAAISTAVAPIERVKLLQVHASKQIAADKQYGIYDCIYR 60
 OY 61 IPREGVLSFWMGNLANVIRYPTQALNFAFDKKYQIPLGGVDKHTQFWRFYAGNLASG 120
 DB 61 IPREGVLSFWMGNLANVIRYPTQALNFAFDKKYQIPLGGVDKHTQFWRFYAGNLASG 120
 OY 121 GAAGATSLCFVYPLDPARFRLAADVKGSGTEREPRGLDCLYKTKRSDGIRLQGFVS 180
 DB 121 GAAGATSLCFVYPLDPARFRLAADVKGSGTEREPRGLDCLYKTKRSDGIRLQGFVS 180
 OY 181 VGGIITRYRAAYGVYDTAKGMLPDPKNTHTIVVSMIAQVTVAVAGVSPFPTVRRMM 240
 DB 181 VGGIITRYRAAYGVYDTAKGMLPDPKNTHTIVVSMIAQVTVAVAGVSPFPTVRRMM 240

RESULT 4
 AAU10380
 ID AAU10380 standard; Protein; 298 AA.
 XX AAU10380;
 AC AAU10380;
 DB 14-FEB-2002 (first entry)
 DE Human adenine nucleotide translocator 3 (ANT3).
 XX Human; adenine nucleotide translocator; ANT;
 KM mitochondrial matrix protein.
 XX Homo sapiens.
 OS WO200185944-A2.
 PN 15-NOV-2001.
 PD 11-MAY-2001; 2001MO-US15416.
 PE 11-MAY-2000; 2000US-0569327.
 PR (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 XX MPI: 2002-055598/07.
 DR N-PSDB; AAS16690.
 DR Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX Example 3; Fig 2; 147bp; English.
 PS The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide, ANT
 CC preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.

XX Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MTEQALSFADFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIADKQKGYVDCIYR 60
1 MTEQALSFADFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIADKQKGYVDCIYR 60
DB 61 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFFAGNLASG 120
61 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFFAGNLASG 120
DB 121 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVYKTKSDGIRGLYOGFSVS 180
121 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVYKTKSDGIRGLYOGFSVS 180
DB 181 VQGIITIRAAVFGVYDTAKGMLDPKNTHTIYVSMIAQVTAAGVSYPEDEVRRMM 240
181 VQGIITIRAAVFGVYDTAKGMLDPKNTHTIYVSMIAQVTAAGVSYPEDEVRRMM 240
DB 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGAGAFVLYVDELKQYI 298
241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGAGAFVLYVDELKQYI 298

RESULT 5

AA041427 ID AA041427 standard; Protein; 323 AA.

AC AA041427;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6358.

XX Human; nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US4263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662391.

XX 19-OCT-2000; 2000US-0683036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AU, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AA160583.

PT Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX Example 2; SEQ ID NO 6358; 1007bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA038642-AA042213) with nocitropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 323 AA:

Query Match 100.0%; Score 1543; DB 22; Length 323;
Best Local Similarity 100.0%; Pred. No. 5.2e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MTEQALSFADFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIADKQKGYVDCIYR 60
26 MTEQALSFADFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIADKQKGYVDCIYR 85
DB 61 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFFAGNLASG 120
86 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFFAGNLASG 145
DB 121 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVYKTKSDGIRGLYOGFSVS 180
146 GAAGATSLCFVYPLDFARTRLADYKSGTEREFGIGDCLVYKTKSDGIRGLYOGFSVS 205
DB 181 VQGIITIRAAVFGVYDTAKGMLDPKNTHTIYVSMIAQVTAAGVSYPEDEVRRMM 240
206 VQGIITIRAAVFGVYDTAKGMLDPKNTHTIYVSMIAQVTAAGVSYPEDEVRRMM 265
DB 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGAGAFVLYVDELKQYI 298
266 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGAMSIVLRGAGAFVLYVDELKQYI 323

RESULT 6

AA018516 ID AA018516 standard; Protein; 298 AA.

XX AA018516;

DT 11-OCT-2002 (first entry)

XX Human insulin receptor signaling modifier SEQ ID NO: 54.

XX Human; insulin receptor signaling; insulin receptor signaling modifier;

XX ISM; diabetes; metabolic syndrome; antidiabetic.

XX Homo sapiens.

OS WO200255664-A2.

PN 18-JUL-2002.

XX 11-JAN-2002; 2002WO-US01048.

XX 12-JAN-2001; 2001US-261226P.

XX 12-JAN-2001; 2001US-261303P.

XX 12-JAN-2001; 2001US-261304P.

XX 12-JAN-2001; 2001US-261335P.

XX 12-JAN-2001; 2001US-261336P.

PR 12-JAN-2001; 2001US-261361P.
PR 12-JAN-2001; 2001US-261456P.
PR 12-JAN-2001; 2001US-261457P.
PR 12-JAN-2001; 2001US-261458P.
PR 12-JAN-2001; 2001US-261459P.
PR 12-JAN-2001; 2001US-261461P.
PR 12-JAN-2001; 2001US-261518P.
PR 12-JAN-2001; 2001US-261531P.
PR 12-JAN-2001; 2001US-261532P.
PR 12-JAN-2001; 2001US-261589P.
PR 12-JAN-2001; 2001US-261590P.
PR 12-JAN-2001; 2001US-261694P.
PR 12-JAN-2001; 2001US-261695P.
PR 12-JAN-2001; 2001US-261697P.
PA (EXEL-) EXELIXIS INC.
PI Seidel-Dugan C, Ferguson KC, Kidd T;
XX WPI; 2002-599664/64.
DR N-PSDB: AAL48635.
XX
XX
PT Identifying an insulin receptor signaling modulator, useful as drug
PT targets for treating diabetes or metabolic disorders, comprises
PT contacting an assay system comprising insulin receptor signaling
PT modifiers with a test agent
XX
XX
PS Disclosure; Page 160-161; 232pp; English.
XX
XX
CC The present invention relates to a method of identifying a candidate
CC Insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.
XX
XX
SQ Sequence 298 AA;
Query Match 94.8%; Score 1463; DB 23; Length 298;
Best Local Similarity 92.9%; Pred. No. 1.8e-148;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTEQAIISPAKDLFLAGIAAISKTAAPLIERVKLLIQVOHASKQIADKQYKGIIVDCIAR 60
DB 1 MTDAAISPAKDLFLAGIAAISKTAAPLIERVKLLIQVOHASKQIADKQYKGIIVDCIAR 60
QY 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQWRFRAGMLASG 120
DB 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQWRFRAGMLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADYVSGTEREFRIGDCLVITKSDGIRGLYGFSSYS 180
DB 121 GAAGATSLCFVYPLDFARTLADYVSGTEREFRIGDCLVITKSDGIRGLYGFSSYS 180
QY 121 GAAGATSLCFVYPLDFARTLADYVSGTEREFRIGDCLVITKSDGIRGLYGFSSYS 180
DB 121 GAAGATSLCFVYPLDFARTLADYVSGTEREFRIGDCLVITKSDGIRGLYGFSSYS 180
QY 181 VGGIILYRAAYFEGVYDTAGMLPDPKNTNTHIVSWMLAQVTAVAGVVSYPEDTVRRMM 240
DB 181 VGGIILYRAAYFEGVYDTAGMLPDPKNTNTHIVSWMLAQVTAVAGVVSYPEDTVRRMM 240
QY 241 QSGRKADIMYTGTCVCMKRIFRDEGGKAFKFKANSNVLRGKAGAVLVLYDELAK 296
DB 241 QSGRKADIMYTGTCVCMKRIFRDEGGKAFKFKANSNVLRGKAGAVLVLYDELAK 296
RESULT 7
AAV71032 standard; Protein; 298 AA.

XX
AC AAV71032;
XX
XX 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT2.
XX
XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
XX mitochondrial permeability transition; neuroprotective; neurotropic;
XX antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
XX antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
XX mitochondrial diabetes and deafness; hyperproliferative disorder;
XX myoclonic epilepsy red ragged fibre syndrome.
XX
XX Homo sapiens.
XX
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1998; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS;
XX
XX WPI; 2000-365619/31.
DR N-PSDB: AAD00520.
XX
XX Recombinant construct encoding adenine nucleotide translocator
XX polypeptide, useful e.g. in screening for potential therapeutic agents
XX against mitochondrial disease
XX
XX Claim 45; Page 172-173; 175pp; English.
PS
XX
XX The patent discloses a method to produce adenine nucleotide translocator
XX (ANT) proteins or ANT fusion proteins using recombinant expression
XX constructs. ANT is a nuclear encoded protein and a major component of
XX inner mitochondrial membrane. It mediates transport of adenosine
XX di/tri-phosphates across the mitochondrial inner membrane and also serves
XX as an important molecular component of the mitochondrial permeability
XX transition pore, a modulator of apoptosis. ANT is used to identify agents
XX or ligands that bind to, or interact with it. The ANT ligands are used to
XX detect or isolate ANT in a biological sample, and therapeutically for
XX regulating mitochondrial pore activity, for treating diseases associated
XX with altered mitochondrial function, including Alzheimer's, Parkinson's
XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
XX disorders, mitochondrial diabetes and deafness (MIND), and myoclonic
XX epilepsy red ragged fibre syndrome. The present sequence is an
XX adenine nucleotide translocator ANT2 from human brain.
XX
XX
SQ Sequence 298 AA;
Query Match 94.2%; Score 1454; DB 21; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MTEQAIISPAKDLFLAGIAAISKTAAPLIERVKLLIQVOHASKQIADKQYKGIIVDCIAR 60
DB 1 MTDAAISPAKDLFLAGIAAISKTAAPLIERVKLLIQVOHASKQIADKQYKGIIVDCIAR 60
QY 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQWRFRAGMLASG 120
DB 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQWRFRAGMLASG 120

Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFEKDYKQIFLGGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTEREFRGLDCLVYTKSDGIRGLYOGFSYS 180
 Db 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTEREFRGLDCLVYTKSDGIRGLYOGFSYS 180
 QY 181 VGGIITRYAAVFGYVDYAKGMLPDPKNTHTIVSWIAQTVAAGVSYEPDVRRRMM 240
 Db 181 VGGIITRYAAVFGYVDYAKGMLPDPKNTHTIVSWIAQTVAAGVSYEPDVRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLYDELRK 296
 Db 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLYDELRK 296

RESULT 8

AAU01199 standard; Protein: 298 AA.

AC AAU01199;

DM 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

KM Human: adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;

KW mitochondrial permeability transition pore component; cell survival;

KM mitochondrial core component; mitochondrial related disorder; cancer;

KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN W0200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US0535.

PR 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Willey SE, Andreyev AV, Frigeri LG;

PI Wellcetebl G, Davis RE;

DR WPI: 2001-291054/30.

DR N-PSDB; AAS05902.

PT New nucleotide acid expression constructs, useful for screening for agents

PT that alter mitochondrial permeability transition (MPT), comprises

PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide

PT fused to energy transfer molecule -

PS Disclosure: Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-2

CC (ANT-2) protein. ANT proteins are mitochondrial permeability

CC transition (MPT) pore components responsible for mediating transport

CC of ADP across the mitochondrial inner membrane. ANT proteins interact

CC with other mitochondrial core components e.g. cyclophilins to

CC regulate MPT. The present invention relates to a novel nucleotide

CC expression construct comprising a promoter operably linked to a

CC polynucleotide encoding a mitochondrial pore component polypeptide

CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein

CC hyperproliferative disorders e.g. cancer, and deafness.

XX SQ Sequence 298 AA;

Query Match 94.2%; Score 1454; DB 22; Length 298;

Best Local Similarity 92.6%; Pred. No. 1.7e-147;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEBQALISFAKDFLAGGIAAIAISKTAVANIERVKLLQVGHASKOITADKQYKGIIDCVR 60
 Db 1 MTEBQALISFAKDFLAGGIAAIAISKTAVANIERVKLLQVGHASKOITADKQYKGIIDCVR 60
 QY 61 IPKEQVLSFWKGNLANVIRYPTQALNFAFEKDYKQIFLGGVDKRTQFWRYFAGNLASG 120
 Db 61 IPKEQVLSFWKGNLANVIRYPTQALNFAFEKDYKQIFLGGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTEREFRGLDCLVYTKSDGIRGLYOGFSYS 180
 Db 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTEREFRGLDCLVYTKSDGIRGLYOGFSYS 180
 QY 181 VGGIITRYAAVFGYVDYAKGMLPDPKNTHTIVSWIAQTVAAGVSYEPDVRRRMM 240
 Db 181 VGGIITRYAAVFGYVDYAKGMLPDPKNTHTIVSWIAQTVAAGVSYEPDVRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLYDELRK 296
 Db 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKAGMSVNLRGMGAFVLYLYDELRK 296

RESULT 9

AAU10379 standard; Protein: 298 AA.

AC AAU10379;

DM 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).

KM Human: adenine nucleotide translocator; ANT; ss;

KW mitochondrial matrix protein.

OS Homo sapiens.

PN W0200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001MO-US15416.

PR 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SW, Szabo TR;

PI Ghosh SS, Moos WH, Pel Y, Carroll AK;

DR WPI: 2002-055598/07.

DR N-PSDB; AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide

PT translocator polypeptides, comprises a regulated promoter linked to

PT nucleotide acid encoding the polypeptide -

PS Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (1)

CC comprising a regulated promoter operably linked to a nucleic acid

CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT

CC proteins mediate the exchange of ADP synthesized in the mitochondrial

CC matrix for ADP in the cytosol. (1) is useful for producing recombinant

ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (1) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT2.
XX
SQ Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 23; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSFANDFLAGGIAAISTKTAVERVLLQVGHASQIADKQKTYDCTYR 60
DB 1 MTDAAISFANKDFLAGGVAIAISTKTAVERVLLQVGHASQIADKQKTYDCTYR 60

QY 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 120
DB 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 120

QY 121 GAAGATSLCFVYPLDFAFRRLADVCKSGTEREFGDLGCLVKTSDGIRGLYGFVSYS 180
DB 121 GAAGATSLCFVYPLDFAFRRLADVCKSGTEREFGDLGCLVKTSDGIRGLYGFVSYS 180

QY 181 VQGIITIRAAFGVYDTAKGMLPDPKNTHTLVSMIAQVTVAVAGVYSYPTDVRRRMM 240
DB 181 VQGIITIRAAFGVYDTAKGMLPDPKNTHTLVSMIAQVTVAVAGVYSYPTDVRRRMM 240

QY 241 QSGRKADIMYGTGTVDCKMRKIFRDEGKAFKFGAMSNVLKMGCAEVLYLDELK 296
DB 241 QSGRKCTDMYGTGTVDCKMRKIADEGKAFKFGAMSNVLKMGCAEVLYLDELK 296

RESULT 10
ABR41715
ID ABR41715 standard; Protein; 429 AA.
XX
XX ABR41715;
AC
XX
XX 02-JUN-2003 (first entry)
DT
XX
XX Human DITHP organelle-associated protein.
DE
XX
XX Human: dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW organelle-associated protein.
XX
XX Homo sapiens.
OS
XX
XX MO200297031-A2.
PN
XX
XX 05-DEC-2002.
PD
XX
XX 27-MAR-2002; 2002MO-US10056.
PF
XX
XX 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Daifo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstlin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
XX WPI: 2003-129518/12.
DR N-PDB: ACC46652.
XX
XX Novel human diagnostic and therapeutic polypeptide useful for
PT identifying test compound which specifically binds to a polypeptide
PT encoded by human diagnostic and therapeutic polynucleotide, and to
PT induce antibodies -
XX
XX Claim 27; SEQ ID No 1250; 591pp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
CC encoded proteins (DITHP: ABR41136-ABR41812). The invention also relates
CC to polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods
CC of detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which is an organelle-
CC associated protein.
CC Note: The sequence data for this patent did not form part of the WPIPO
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX
SQ Sequence 429 AA;

Query Match 91.9%; Score 1418; DB 24; Length 429;
Best Local Similarity 95.2%; Pred. No. 2e-143;
Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;

QY 1 MTEQATSFANDFLAGGIAAISTKTAVERVLLQVGHASQIADKQKTYDCTYR 60
DB 26 MTEQATSFANDFLAGGIAAISTKTAVERVLLQVGHASQIADKQKTYDCTYR 85

QY 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 120
DB 86 IPKEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 145

QY 121 GAAGATSLCFVYPLDFAFRRLADVCKSGTEREFGDLGCLVKTSDGIRGLYGFVSYS 180
DB 146 GAAGATSLCFVYPLDFAFRRLADVCKSGTEREFGDLGCLVKTSDGIRGLYGFVSYS 205

QY 181 VQGIITIRAAFGVYDTAKGMLPDPKNTHTLVSMIAQVTVAVAGVYSYPTDVRRRMM 240
DB 206 VQGIITIRAAFGVYDTAKGMLPDPKNTHTLVSMIAQVTVAVAGVYSYPTDVRRRMM 265

OY 241 OSGRKADIMYTGTVDCMRKIFRDEGKAFKGA-W-----SNVLRGMGCA 285
 |||||||
 Db 266 OSGRKADIMYTGTVDCMRKIFRDEGKAFKGA-FGSHMKQATLADLEGSPSA 316
 |||||||
 RESULT 11
 ID AAM61169 standard; Protein; 298 AA.
 XX AAM61169;
 AC
 DT 28-SEP-1998 (first entry)
 DE
 DE Anti protein.
 XX
 XX Anti; Adenine nucleotide translocator; cloning; screening;
 KM DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
 KM Probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 KM hyperlactic acidosis; degenerative muscle disease.
 KM lactic acidosis; degenerative muscle disease.
 XX
 OS Mus sp.
 XX WC9819714-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 31-OCT-1997; 97WO-US19882.
 XX
 PR 01-NOV-1996; 96US-0030017.
 XX
 PA (UYEM-) UNIV EMORY.
 PI
 PI Graham BC, Macgregor GR, Wallace DC;
 DR WPI: 1998-286608/25.
 DR N-PSDB: AAV36479.
 XX
 XX Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hyperlactic
 PT cardiomypathy in animals and to test therapeutic compositions or
 PT gene therapies
 PS
 PS Disclosure: Page 39-40; 61pp; English.
 XX
 XX The present sequence is the mouse Anti protein, the cDNA producing this
 CC polypeptide is cloned by screening a mouse heart cDNA library with the
 CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
 CC Tag dideoxy terminator cycle sequencing. The Anti protein is encoded by
 CC the Anti locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Anti homozygous mutant would
 CC be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Anti homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hyperlactic acidosis, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of ANT1.
 CC
 SQ Sequence 298 AA:
 Query Match 91.5%; Score 1412; DB 19; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5,4e-143;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 OY 1 MTEQAFKDFLAGIAAISTAVAPIERVKLLQVQHSKQIADQYKIVCIYR 60
 |||||||
 Db 1 MDDQALSPKDFLAGIAAIVSKTAVAPIERVKLLQVQHSKQISEKQYKIIDCVVR 60
 |||||||
 OY 61 IPKEGVFSEWRGLANVIRYPTQALNFAFDKXKQIIFLGVDYDKHOFRRYRAGTASG 120
 |||||||
 Db 61 IPKEGVFSEWRGLANVIRYPTQALNFAFDKXKQIIFLGVDYDKHOFRRYRAGTASG 120
 |||||||

OY 121 GAAGATSLCFVYPLDPAFTRLADADVCKSGTEREPRGIGDCLVITKSDGIRGLYQGFSEVS 180
 |||||||
 Db 121 GAAGATSLCFVYPLDPAFTRLADADVCKSGTEREPRGIGDCLVITKSDGIRGLYQGFSEVS 180
 |||||||
 OY 181 VOGIIIRAAVFEGVYDTAKGMLPDKRNTHIVSWMIMQVTAAGVASYPEDTYRRRAMM 240
 |||||||
 Db 181 VOGIIIRAAVFEGVYDTAKGMLPDKRNTHIVSWMIMQVTAAGVASYPEDTYRRRAMM 240
 |||||||
 OY 241 OSGRKADIMYTGTVDCMRKIFRDEGKAFKGA-SVNLKMGCAFVLVYDELKRV 298
 |||||||
 Db 241 OSGRKADIMYTGTVDCMRKIFRDEGKAFKGA-SVNLKMGCAFVLVYDELKRV 298
 |||||||
 RESULT 12
 ID AB053219 standard; Protein; 293 AA.
 XX AB053219;
 AC
 DT 14-APR-2003 (first entry)
 DE
 DE Human metabolism-associated DKFZphes3_35n12 homologue #1.
 KM Human; gene therapy; vaccine; disease treatment; detection.
 KM Homo sapiens.
 OS
 XX WO200112659-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000MO-IB01496.
 XX
 PR 18-AUG-1999; 99US-0149499.
 XX
 PR 28-SEP-1999; 99US-0156503.
 XX
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 PI
 PI Wiemann S;
 DR WPI: 2001-327840/34.
 XX
 XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies -
 PT
 PS Example III: Page 850; 1095pp; English.
 XX
 XX This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.
 CC
 SQ Sequence 293 AA:
 Query Match 91.1%; Score 1406; DB 22; Length 293;
 Best Local Similarity 90.1%; Pred. No. 2.3e-142;
 Matches 263; Conservative 17; Mismatches 12; Indels 0; Gaps 0;
 OY 5 AISPARKDFLAGIAAISTAVAPIERVKLLQVQHSKQIADQYKIVCIYRIPKE 64
 |||||||
 Db 1 ALSPKDFLAGIAAIVSKTAVAPIERVKLLQVQHSKQISEKQYKIIDCVRIPIKE 60
 |||||||
 OY 65 OGVLSEFWRGLANVIRYPTQALNFAFDKXKQIIFLGVDYDKHOFRRYRAGTASG 124
 |||||||
 Db 61 OGVLSEFWRGLANVIRYPTQALNFAFDKXKQIIFLGVDYDKHOFRRYRAGTASG 120
 |||||||

QY 125 ATSLCPVPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVSGI 184
 Db 121 ATSLCPVPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVSGI 180
 QY 185 IYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVYTAAGVYSPEDVRRRRMMQSGR 244
 Db 181 IYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVYTAAGVYSPEDVRRRRMMQSGR 240
 QY 245 KGADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLRGMGAFVLVYDELK 296
 Db 241 KGADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLRGMGAFVLVYDEIKK 292
 RESULT 13
 AAY71031
 ID AAY71031 standard; Protein; 297 AA.
 XX AAY71031;
 AC AAY71031;
 XX 29-ADG-2000 (first entry)
 DT
 XX Human adenine nucleotide translocator ANT1.
 DE
 XX Human: adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; neurotoxic;
 KM antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KM antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS
 XX WO200026370-A2.
 PN 11-MAY-2000.
 PD
 XX 03-NOV-1999; 99WO-US25883.
 PF
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 XX (MITO-) MITOKOR.
 PA
 XX Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
 PI Ghosh SS;
 DR MPI; 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PT
 XX Claim 44; Page 172; 175pp; English.
 PS
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, MELAS, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MTEQAIISFAKDLFLAGIAAISKTAAPIERKLLIQVHASKQISAEKQYGIIDCVYR 60
 Db 1 MGDHAWSEFLKDFLAGAAVAASKTAPIERKLLIQVHASKQISAEKQYGIIDCVYR 60
 QY 61 IPKEQGVLSFWRGNTLANVIRYPTQALNFAFKDKYKQIFAGVGDVHTQFRRYFAGNLASG 120
 Db 61 IPKEQGVLSFWRGNTLANVIRYPTQALNFAFKDKYKQIFAGVGDVHTQFRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFAFRRLADVGKSGTEREERGLGDCLVKTKSDGIRGLYOGFSVS 179
 QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVYTAAGVYSPEDVRRRRMM 240
 Db 180 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQVYTAAGVYSPEDVRRRRMM 239
 QY 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLRGMGAFVLVYDELK 298
 Db 240 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLRGMGAFVLVYDEIK 297
 RESULT 14
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX AAU01198;
 AC AAU01198;
 XX 07-SEP-2001 (first entry)
 DT
 XX Human adenine nucleotide translocator-1 (ANT-1) protein.
 DE
 XX Human: adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO200132876-A2.
 PN 10-MAY-2001.
 PD
 XX 03-NOV-2000; 2000WO-US30535.
 PF
 XX 03-NOV-1999; 99US-0434354.
 PR
 XX (MITO-) MITOKOR.
 PA
 XX Murphy AN, Clevenger W, Willey SE, Andreyev AV, Fritger LG;
 PI Vellelebi G, Davis RE;
 DR MPI; 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PT
 XX Disclosure; Fig 2; 186pp; English.
 PS
 XX The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability

CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 297 AA:

Query Match 89.8%; Score 1385.5; DB 22; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQATSPANDFLAGIAAISTAVAPIERVKLLLOVHASKOIADKOYICVDCYR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGLDCYVR 60
 QY 61 IPKQGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDNHTQFMRFRAGNLASG 120
 DB 61 IPKQGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDNHTQFMRFRAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFAFRTLAADVGRSRETEREGLDGCLVTKITKSDGIRGLYOGFSYS 180
 DB 121 GAAGATSLCFEYPLDFAFRTLAADVGRSRETEREGLDGCLVTKITKSDGIRGLYOGFSYS 179
 QY 181 VGGIIYRAAYEGYVDIAKGMIPDKNTHIVSMIAQVTAVAGVSYPPDIYRRRMM 240
 DB 180 VGGIIYRAAYEGYVDIAKGMIPDKNTHIVSMIAQVTAVAGVSYPPDIYRRRMM 239
 QY 241 QSGRGADIMYTGTVDCWKRIKADGAKAFKGAWSNVLKMGGAFLVLYDELKKYV 298
 DB 240 QSGRGADIMYTGTVDCWKRIKADGAKAFKGAWSNVLKMGGAFLVLYDELKKYV 297

RESULT 15

AAU10378 standard: Protein: 297 AA.

XX AAU10378:

XX 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 1 (ANT1).

XX Human: adenine nucleotide translocator; ANT;

XX mitochondrial matrix protein.

XX Homo sapiens.

XX MO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001MO-US15416.

XX 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 XX Ghosh SS, Moos WH, Pel Y, Carroll AK;

DR WPI: 2002-055598/07.

DR N-PSDB; AAS16688.

XX Novel recombinant expression construct for producing adenine nucleotide

XX translocator polypeptides; comprises a regulated promoter linked to

XX nucleic acid encoding the polypeptide

Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (1)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (1) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT1.

XX Sequence 297 AA:

Query Match 89.8%; Score 1385.5; DB 23; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQATSPANDFLAGIAAISTAVAPIERVKLLLOVHASKOIADKOYICVDCYR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGLDCYVR 60
 QY 61 IPKQGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDNHTQFMRFRAGNLASG 120
 DB 61 IPKQGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDNHTQFMRFRAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFAFRTLAADVGRSRETEREGLDGCLVTKITKSDGIRGLYOGFSYS 180
 DB 121 GAAGATSLCFEYPLDFAFRTLAADVGRSRETEREGLDGCLVTKITKSDGIRGLYOGFSYS 179
 QY 181 VGGIIYRAAYEGYVDIAKGMIPDKNTHIVSMIAQVTAVAGVSYPPDIYRRRMM 240
 DB 180 VGGIIYRAAYEGYVDIAKGMIPDKNTHIVSMIAQVTAVAGVSYPPDIYRRRMM 239
 QY 241 QSGRGADIMYTGTVDCWKRIKADGAKAFKGAWSNVLKMGGAFLVLYDELKKYV 298
 DB 240 QSGRGADIMYTGTVDCWKRIKADGAKAFKGAWSNVLKMGGAFLVLYDELKKYV 297

Search completed: August 18, 2003, 16:11:32
 Job time : 85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:09:02 ; Search time 42 Seconds
(without alignments)
682,340 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEOAIISFAKDFLAGGIAAA.....LNGMGATVLYIDELKKVI 298

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	1 S03894	ADP, ATP carrier pr
2	1512	98.0	298	2 B43646	ADP, ATP carrier pr
3	1454	94.2	298	1 A29132	ADP, ATP carrier pr
4	1424	92.3	298	2 T60173	adenine nucleotide
5	1422	92.2	298	1 XWBO	ADP, ATP carrier pr
6	1418	91.9	298	2 S37210	ADP, ATP carrier pr
7	1409	91.3	298	1 A44778	ADP, ATP carrier pr
8	1405	91.1	298	2 S31814	ADP, ATP carrier pr
9	1184	76.7	301	1 S31935	ADP, ATP carrier pr
10	1041	67.5	313	2 T23207	hypothetical prote
11	1039	67.3	313	2 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP, ATP carrier pr
15	943	61.1	301	2 S51132	ADP, ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP, ATP carrier pr
17	772	50.0	308	1 S30259	ADP, ATP carrier pr
18	769	49.8	322	2 T40526	ADP, ATP carrier pr
19	768	49.8	386	2 T09709	ADP, ATP carrier pr
20	766	49.5	313	1 XWMC	ADP, ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP, ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP, ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14974	ADP, ATP carrier pr
26	748	48.5	386	2 S21974	ADP, ATP carrier pr
27	747	48.4	306	2 T42011	ADP, ATP carrier pr
28	747	48.4	386	2 S17917	ADP, ATP carrier pr
29	744	48.2	387	2 S16586	ADP, ATP carrier pr

30	743	48.2	379	2 T04608	ADP, ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP, ATP carrier pr
32	742	48.1	382	2 S33630	ADP, ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP, ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP, ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP, ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	2	T51577	ADP, ATP translocas
38	383	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	mitochondrial solu
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.5	475	2 T50686	peroxisomal Ca-dep
44	363	23.8	44	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

ADP, ATP carrier protein T3 - human
N/Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP,
C/Species: Homo sapiens (man)
C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C/Accession: S03894; B28116
R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.
T_MOL Biol 206, 261-280, 1989

A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A/Reference number: S03893; MUID:89236396; PMID:2541251
A/Accession: S03894

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-298 <COZ>

R/Houlsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1

A/Reference number: A94197; MUID:88124845; PMID:2829183

A/Accession: B28116

A/Molecule type: mRNA

A/Residues: 36-104, 'R', '106', 'A', '109-298 <HOU>

A/Cross-references: GB:003592; NID:9339722; PIDN:AAA36750.1; PID:9339723

A/Experimental source: liver

C/Genetics:

A/Genes: GDB:AMT3; AMT3Y

A/Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A/Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A/Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and G

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP, ATP carrier protein #status predicted <MAT>

F:5-99/Dominant: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Dominant: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Dominant: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 66-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEOAIISFAKDFLAGGIAAISKTAAPVIRVLLQLQVHASKQIADKQYGVDCIVR	60
DB	1	MTEOAIISFAKDFLAGGIAAISKTAAPVIRVLLQLQVHASKQIADKQYGVDCIVR	60
QY	61	IPKEQGLVSRWGNLANVITFPQALNFAFKKQKQIFLGVDKHTQFRFRAGNLASG	120
DB	61	IPKEQGLVSRWGNLANVITFPQALNFAFKKQKQIFLGVDKHTQFRFRAGNLASG	120
QY	121	GAAGATSLCFVYPLDFARTRLADVKGSGEREFRGLDCLVTKTSKDGIRGLYOGPSVS	180
DB	121	GAAGATSLCFVYPLDFARTRLADVKGSGEREFRGLDCLVTKTSKDGIRGLYOGPSVS	180

OY 181 VGGIIIRAAFGVYDTAKGMLDPKRNTHIVSMIAQTVAVAGVSYFEDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFGVYDTAKGMLDPKRNTHIVSMIAQTVAVAGVSYFEDTVRRMM 240
 OY 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKRYI 298
 |||
 Db 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKRYI 298

RESULT 2

ADP/ATP carrier protein T2 - bovine
 A:Accession: B43646
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 R:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 BiochemJ 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <PRO>

A:Cross-references: GB:M4103; NID:9529416; PID:AAA30769.1; PID:9529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 98.08; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.78; Pred. No. 3, 3e-126;
 Matches 291; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGIAAISKTAAPATERVKLLQVHASKQIADKQKIVDCIVR 60
 |||
 Db 1 MTEQAISFAKDFLAGIAAISKTAAPATERVKLLQVHASKQIADKQKIVDCIVR 60
 OY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 |||
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLADVKGSGTEREFGIGDCLVTKTSKDSGIRGLYOGFVS 180
 |||
 Db 121 GAAGATSLCFYPLDFARTRLADVKGSGTEREFGIGDCLVTKTSKDSGIRGLYOGFVS 180
 OY 181 VGGIIIRAAFGVYDTAKGMLDPKRNTHIVSMIAQTVAVAGVSYFEDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFGVYDTAKGMLDPKRNTHIVSMIAQTVAVAGVSYFEDTVRRMM 240
 OY 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKRYI 298
 |||
 Db 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKRYI 298

RESULT 3

ADP/ATP carrier protein T2 - human
 A:Accession: A29132
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 R:Accession: A29132; C28116
 R:Battni, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>

A:Cross-references: GB:J02683; NID:9179246; PID:AAA35579.1; PID:9179247
 R:Houseworth, J.; Atarashi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:9339720; PID:AAA36749.1; PID:9339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; ZP1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-q26
 A:Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 94.28; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.08; Pred. No. 4, 5e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGIAAISKTAAPATERVKLLQVHASKQIADKQKIVDCIVR 60
 |||
 Db 1 MTEQAISFAKDFLAGIAAISKTAAPATERVKLLQVHASKQIADKQKIVDCIVR 60
 OY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 |||
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFGAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLADVKGSGTEREFGIGDCLVTKTSKDSGIRGLYOGFVS 180
 |||
 Db 121 GAAGATSLCFYPLDFARTRLADVKGSGTEREFGIGDCLVTKTSKDSGIRGLYOGFVS 180
 OY 181 VGGIIIRAAFGVYDTAKGMLDPKRNTHIVSMIAQTVAVAGVSYFEDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFGVYDTAKGMLDPKRNTHIVSMIAQTVAVAGVSYFEDTVRRMM 240
 OY 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKRYI 298
 |||
 Db 241 OSGRGADIMYTGIVDCMKRIFDEGKAFKFGAMSNVLRMGCAFVLYLYDELKRYI 298

RESULT 4

adenine nucleotide translocator - rat
 A:Accession: 160173
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 R:Shiohara, T.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: 160173; MUID:94002161; PMID:8399300
 A:Accession: 160173
 A:Status: Preliminary; translated from GB/EMBL/DD83

A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:9400426; PID:CAA3842.1; PID:9400427
 C:Genetics:
 A:Gene: anti
 A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 92.38; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.68; Pred. No. 2e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGIAAISKTAAPATERVKLLQVHASKQIADKQKIVDCIVR 60
 |||
 Db 1 MTEQAISFAKDFLAGIAAISKTAAPATERVKLLQVHASKQIADKQKIVDCIVR 60

QY 61 IPKRGVGLTFSPWRGLNAVIVYFPFQALNPAFKPKYKRIPLFGVDKTHQFRRYRAGNLSG 120

Db 61 IPKRGVGLTFSPWRGLNAVIVYFPFQALNPAFKPKYKRIPLFGVDKTHQFRRYRAGNLSG 120

QY 121 GAAGATSLCFYVPLDFFARTRLAADVSGKGEREREGIGDCLVTKTSKDGIRGIXYOGFSVS 180

Db 121 GAAGATSLCFYVPLDFFARTRLAADVSGKSSQORENGIGDCLTKIFKSDGLKGLXQGFVS 180

QY 181 VGGIITRYAAVFGVYDTAKGMLPDPKNTHTIVSMMLAQTVATAVAGVSVYPDFVRRMM 240

Db 181 VGGIITRYAAVFGVYDTAKGMLPDPKNTHTIVSMMLAQTVATAVAGVSVYPDFVRRMM 240

QY 241 QSGRRKADIMYTCGVDDCKRIKFRDEGKRAFFKGMNVLAGMGAFVLVLYDELKRYI 298

Db 241 QSGRRKADIMYTCGVDDCKRIKFRDEGKRAFFKGMNVLAGMGAFVLVLYDELKRYI 298

RESULT 5

XMB0

ADP/ATP carrier protein T1 - bovine

N:Alternate names: ADP/ATP translocase T1

C:Species: Bos primigenius taurus (cattle)

C:Date: 14-Nov-1993 #sequence,revision 22-Jul-1994 #text_change 22-Jun-1999

C:Accession: A43646; A24822; A03181; A61343; S69369

C:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

BiochemJ 20, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in

A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: A43646

A:Molecule type: mRNA

A:Residues: 1-298 <PM>

A:Cross-references: GB:M4102; NID:g529414; PIDN:AAA30768.1; PID:g529415

R:Rasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual

A:Reference number: A24822; MUID:86295775; PMID:3017341

A:Accession: A24822

A:Molecule type: mRNA

A:Residues: 208-298 <RAS>

A:Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631

R:Ragulla, H.; Misra, D.; Eulitz, M.; Klingenberg, M.

Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982

A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondr

A:Reference number: A03181; MUID:82188267; PMID:7076130

A:Accession: A03181

A:Molecule type: protein

A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AQU>

A>Note: residue 52 may be methyllysine

R:Babel, W.; Wachter, E.; Agulla, H.; Klingenberg, M.

Biochim. Biophys. Acta 670, 176-180, 1981

A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoct

A:Reference number: A61343; MUID:82046806; PMID:6271240

A:Accession: A61343

A:Molecule type: protein

A:Residues: 205-298 <BAB>

R:Oetmeier, W.; Masson, K.; Kalinna, S.

Eur. J. Biochem. 227, 730-733, 1995

A:Title: [(3)H]-azido-4-isopropylaziridone labels Cys159 of the bovine mitochondrial ADP

A:Reference number: S69369; MUID:95172038; PMID:7867632

A:Accession: S69369

A:Molecule type: protein

A:Residues: 49-63;154-168 <OET>

C:Comment: This protein is synthesized in the cytosol and transported into the mitochondr

C:Complex: homodimer

C:Function:

A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera

A>Note: Located in the inner mitochondrial membrane

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch

F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

```

F:52/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F:52/Modified site: N6-methyllysine (lys) #status predicted

Query Match          92.2%; Score 1422; DB 1; Length 298;
Best Local Similarity 89.3%; Pred. No. 3..1e-118;
Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQALISFANDFLAGGIAAIAISKTAVPIERVKLLQVGHASKQIADQKYGIVDCIVR 60
DB 1 MSDQALSFLEDFLAGGIAAIAISKTAVPIERVKLLQVGHASKQISAEKQYGIIDCVRR 60
QY 1PKRGQGLSFWRGNLANVIRFPQALNFAFKKYYKQIFLGVDNRHOFKRYRAGNIAAG 120
DB 1PKRGQGLSFWRGNLANVIRFPQALNFAFKKYYKQIFLGVDNRHOFKRYRAGNIAAG 120
QY 121 GAAGATSLCFEYPLDFEARTRLAADVCKSGEREFRGLGDCLVYITRSDSIRGLYQGSFYS 180
DB 121 GAAGATSLCFEYPLDFEARTRLAADVCGAQRREFTGLGNQITRIFRSDLRGLYQGSFNS 180
QY 181 VQGIITIRAAVFGYVDPAKGMLDPPKNTHTIVSMIAQTAVAGVSYSPEDTVRRRMM 240
DB 181 VQGIITIRAAVFGYVDPAKGMLDPPKNTHTIVSMIAQTAVAGVSYSPEDTVRRRMM 240
QY 241 QSGRRGADIMTGTGVDCWRKIFRDEGSKAFPKGAMSNTVLRGMGAFVLVLYDELKVI 298
DB 241 QSGRRGADIMTGTGVDCWRKIADEGSKAFPKGAMSNTVLRGMGAFVLVLYDELKVF 298

RESULT 6
S37210
ADP,ATP carrier protein T1 - mouse
N:Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence,revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S37210
R:Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 1993
A:Reference number: S37210
A:Accession: S37210
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1*298 <LAP>
A:Cross-References: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
A:Genetics:
A:Gene: ANCI
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
P:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
P:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
P:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match          91.9%; Score 1418; DB 2; Length 298;
Best Local Similarity 88.9%; Pred. No. 6..9e-118;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQALISFANDFLAGGIAAIAISKTAVPIERVKLLQVGHASKQIADQKYGIVDCIVR 60
DB 1 MGDQALSLFKDLFLAGGIAAIAVSKTAVPIERVKLLQVGHASKQISAEKQYGIIDCVRR 60
QY 61 IPKRGQGLSFWRGNLANVIRFPQALNFAFKKYYKQIFLGVDNRHOFKRYRAGNIAAG 120
DB 61 IPKRGQGLSFWRGNLANVIRFPQALNFAFKKYYKQIFLGVDNRHOFKRYRAGNIAAG 120
QY 121 GAAGATSLCFEYPLDFEARTRLAADVCKSGEREFRGLGDCLVYITRSDSIRGLYQGSFYS 180
DB 121 GAAGATSLCFEYPLDFEARTRLAADVCGAQRREFTGLGNQITRIFRSDLRGLYQGSFNS 180
QY 181 VQGIITIRAAVFGYVDPAKGMLDPPKNTHTIVSMIAQTAVAGVSYSPEDTVRRRMM 240
DB 181 VQGIITIRAAVFGYVDPAKGMLDPPKNTHTIVSMIAQTAVAGVSYSPEDTVRRRMM 240
QY 241 QSGRRGADIMTGTGVDCWRKIFRDEGSKAFPKGAMSNTVLRGMGAFVLVLYDELKVI 298
DB 241 QSGRRGADIMTGTGVDCWRKIFRDEGSKAFPKGAMSNTVLRGMGAFVLVLYDELKVF 298

```


F;112-204/Domain:	ADP,ATP carrier protein repeat	homology	<ACP2>
F;209-300/Domain:	ADP,ATP carrier protein repeat	homology	<ACP3>

Query Match	76.7%;	Score 1184;	DB 1;	Length 301;
Best Local Similarity	77.0%;	Pred. NO. 3.6e-97;		
Matches 231; Conservative	23;	Mismatches 44;	Indels 2;	Gaps 1

QY	1	IMEQA--ISFADPLAGIGIAAISTTAAPLERKLLLOVOMASKOIAADKQYKGIYDCI	58
Db	1	MRKADPYFADPLAGIGISAAVSTKANAPERKLLLOVOMASKOIAADKQYKGIYDCI	60
QY	59	VRIPKQGVLSFWKGNLANVIRPEPQALNAPFKDKYKQIFLGSVDKHTQFWRYEAGNLA	118
Db	61	VRIPKBOGIGAGCGGNLANVIRPEPQALNAPFDVYKQVFLGSDVDKNTQFWRYEAGNLA	120
QY	119	SGCAATSLCYVYPLDFARTPLADVKSQSTEREPEFLGDCIYKIRKSGINGIYOGFS	178
Db	121	SGCAATSLCYVYPLDFARTPLADVCPGAGEREPEFLGDLCLKYKSDGIIIGLIRGFN	180
QY	179	VSVQGIIRAYFQVYDTAKGMLPDPKNTIIVVSMIAQIVTVAVAGVSPEDTVRRM	238
Db	181	VSVQGIIRAYFQCEPFAKMLPDPKNTSIFSMIAQIVTVASGIIISYEPDTVRRM	240
QY	239	MMQSGKSGADIVYTFVQCMRKIRFEDBECKRPFEGAMSNYLRGGAFFLYLIDELKVI	298
Db	241	MMQSPCKSEVMKNTLQDQWALIGQBOSSGAFEGASNVNLRGGAFFLYLIDELKVI	300

RESULT 10

hypothetical protein K01H12.2 - *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19707
A:Accession: T23207
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <WIL>
A:Cross-references: EMBL:Z68218; PIDN:CMA92472.1; GSPDB:GN00022; CESP:K01H12.2
A:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1, 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

	Query Match	Best Local Match	Similarity	Conservative	Score	DB	Length	Indels	Gaps
	Query Match	Best Local Match	Similarity	Conservative	Score	DB	Length	Indels	Gaps
	Matches	207	70.9%	29	1041	DB 2	313	52	4
					1.7e-84				3
QY	8	FAKFDLAGGIAAISKTA	VAPIERKLLIQVOHASKQIAADK	ROYKGIYD	YVIRPREGV	67			
		: :							
Db	25	FLIDLASGTTAAASKTA	VAPIERKLLIQVODASLT	TAADKRYGIDV	LYAVREKGY	84			
QY	68	LSFMRGNLANVIRYEP	TQALNFAFKDKYQJIF	LGGVDKHTQFWR	FAGNLASGAAGATS	127			
		: : : : :							
Db	85	AALMRGNLANVIRYEP	TQALNFAFKDQYKJIF	QKDLDDKDPK	FWKFAAGNLASGAAGATS	144			
QY	128	LCFVYPLDFAATRI	LAADVGKSGTEREP	FGLDGCLVTK	ISDGI	IRGLYOGFSV	VOGIITY	187	
Db	145	LCFVYPLDFAATRI	LAADVGKA - NERE	EPFGILADCLV	KIAKSDP	IGLGRF	FEVVOGIITY	203	
QY	188	RAAFEGVYDTRAKGM	-PDPKNTHTIVSMM	IAQTYA	VAGVSY	PPEDTYARRMM	MGSRKG	246	
Db	204	RAAFEGMFDTRAKM	FTADGKLNFEPA	AAIAQVAV	YVSGSIISY	PMDTYARRMM	MGSGRK -	262	
QY	247	ADINVTGVDQWRI	FEDEGGKAFKFG	AMSANTL	RCMGK	FGVLYLV	LDLKKVY	298	
Db	263	-DVLEKNTLDA	CAVKTIRNEG	SAMKGA	LSINFR	GTGGLV	LAITAYIDE	LOKFI	313

RESULT 11
T25850

T25850

hypothetical protein TUB11.4 - *Caenorhabditis elegans*

C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:/Accession: T25850
R/Geisels, C.; Stelljes, L.
submitted to the EMBL Data Library, December 1996
A:/Description: The sequence of C. elegans cosmid T01B11.
A:/Reference number: Z20099
A:/Accession: T25850
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: DNA
A:/Residues: 1-313 <GRT>
A:/Cross-references: EMBL:U080931; PDB:1AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A:/Experimental source: strain Bristol N2; clone T01B11
C:/Gene: CESP:T01B11.4
C:/Genetics:
A:/Gene: CESP:T01B11.4
A:/Map position: 4
A:/Introns: 4/1. 191/2
C:/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

[illegible]

RESULT 12

T25371

hypothetical protein WZ/E9.1 - *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20024
A:Accession: T25371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <MII>
A:Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1
A:Experimental source: clone T27E9
C:Genetics:
A:Gene: CESP:T27E9.1
A:Map position: 3
A:Introns: 20/1; 41/3; 115/2
C:Superfamily: ADP/ATP carrier protein; ADP,ATP carrier protein repeat homology

```

0Y 8 FALDFLAGGIAAIAISTAVAPIERVKLLQVHASKIADKROYKIGVDCIYIPRECOV 67
Db 12 FLIDLASGGHAAAVSTAVAPIERVKLLQVQDASKALVADNRKIGIMVLIJVPREGCV 71
0Y 68 LSPMRNGLNVIRYPTOLANLPAFKDYKQJFELGSGVRRHOFMRHYFNGINLAASGAAGNS 127
Db 72 AALMRGNLANVIRYPTOLANLPAFKDYKQJFELGSLDRKNDPFKFPAGNLAASGAAGNS 131
0Y 128 LCVYVYLPDAPRRRIADVNGSGTEREPGLDCCVKTETKDGIRGLYOGSVYOGIIYY 187
Db 132 LCVYVYLPDAPRRRIADVNGSGTEREPGLDCCVKTETKDGIRGLYOGSVYOGIIYY 190
0Y 188 RAAVECVYLPDAGML-POPKNTHIVSMKIQVTANAVGVSVSTPEQIVRRRMMQSGRKG 246
Db 191 RAAVEGVETPAKKVAPASDQGLNFPFPAAGLQVYTVSGSLTSPMDIVRRRMMQSGRKG- 249
0Y 247 ADIMHYGVYDCKRKIFRDBCGKAPFKGMSNVILGNGKGVYLVLYDELKVI 298
Db 250 -DLIKNTLDCAKTIIQNGMSAMFKGALSVNFGTSGALVLAIVYDIQCFL 300

```

```

RESULT 13
T15206
hypothetical protein W02D3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T15206
R:Le, T.; Weinstein, L.; Rifkin, L.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid W02D3.
A:Reference number: Z18908
A:Status:partial
A:Stem:100
A:Molecule type: DNA
A:Residues: 1-300 <EET>
A:Cross-references: EMBL:AF003141; NID:q2088732; PID:q2088738; PIND:AB54179.1; GSPDB:G
C:Genetics:
A:Experimental source: strain Bristol N2; clone W02D3
C:Gene: CESP:W02D3.6
A:Map position: 1
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier repeat homology <ACNR>
F:9-103/Domain: ADP/ATP carrier repeat homology
Query Match 64.4%; Score 993.5; DB 2; Length 300;
Best Local Similarity 64.8%; Pred. No. 2.6e-80;
Matches 199; Conservative 40; Mismatches 59; Indels 7; Gaps 4;

```

QY	2	TEOAISFAR---	DELAGGIAAIAISKRTAAVAPERKLLQYVHMSKOIADKROYGVDCI	58
Db	3	TKGCFYRRFLVDLASG	GTAAAIKSTVAAPIERVKLLQYVSDSEYETVADKKYKIMDVL	62
QY	59	VRIPKBOGVLSEFWRG	LNANVIRYFPTQALNFAEFDKKYQJFLGQVAVKHQFWMFYFAGNIA	118
Db	63	ARPKKOGAAATWRG	LNANLVNRYFPTQALNFAEFDKKYQJFLGQVAVKHQFWMFYFAGNIA	122
QY	119	SGGAGATSLCFYV	PLDPARTRLADAVGKSTEEFERGLDCLVKTIKSDGIRGLYOGFS	178
Db	123	SGVAGATSLCFYV	PLDPARTRLADAVGKSTEEFERGLDCLVKTIKSDGIRGLYOGFS	181
QY	179	VSVOGIIIRAAV	ECVYDPAKGL--PDQRKNTHIVFSMIIKOYTANAGVSVPEQVRRR	237
Db	182	VSVOGIIIRAAV	ECVYDPAKGL--PDQRKNTHIVFSMIIKOYTANAGVSVPEQVRRR	241
QY	238	MMHQSRKADIMY	QVDCMKRIKPRDGGCGAFPKGAMSVNLGCMGCAVILVYDELRKV	297
Db	242	MMHQSGRK--	DILYKNTLDCVARIKIVNEGITALYKGLSNVFATGALVLTLYDEIOHL	299
QY	298	I	298	
Db	300	I	300	

RESULT 14

A41677
ADP, ATP carrier protein - *Chlorella kessleri*
C.Specties: *Chlorella kessleri*
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #ext_change 20-Aug-1999
C.Accession: A41677
R.HilgartH. C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 265: 24044-24047, 1991
R.Title: Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde 3-phosphate dehydrogenase in *Chlorella kessleri*
A.Reference number: A41677, M0ID:92084708, PMID:1748677
A.Accession: A41677
A.Status: Preliminary
A.Molecule type: mRNA
A.Residues: 1-339 <HL>
A.Cross references: G6:M76669; NID:9516596; PIDD:AAA33027.1; PID:9516597
C.Specificity: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C.Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:38-134/domain: ADP, ATP carrier protein repeat homology <ACPI>
F:114-135/domain: ADP, ATP carrier protein repeat homology <AC2>
F:241-329/domain: ADP, ATP carrier protein repeat homology <AC3>

[illegible]

ADP/ATP carrier protein - malaria parasite (Plasmodium falciparum)
N:Alternate names: ADP/ATP transporter
C:Species: Plasmodium falciparum
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C:Accession: S68993; S51132
C:Haftin, I.; Jaureguiberry, G.
Eur. J. Biochem. 228, 86-91, 1995
A:Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human ma
A:Reference number: S68993; M0ID:95188918; PMID:7883016
A:Accession: S68993
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-301 <ADP>
A:Superfamily: ADP/ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:6-103/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F:112-203/Domain: ADP/ATP carrier protein repeat homology <AC2>
F:209-301/Domain: ADP/ATP carrier protein repeat homology <AC3>

Query Match 61.1%; Score 943; DB 2; Length 301;
Best Local Similarity 61.8%; Pred. No. 7.6e-76;
Matches 183; Conservative 45; Mismatches 62; Indels 6; Gaps 5;

2

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:02:07 ; Search time 24 Seconds

(without alignments)
583,915 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQALSPKADFLAGCIANA.....LNGMGAPVLYLDELKVIY 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1	ADT3_HUMAN*
2	1512	98.0	298	1	ADT3_BOVIN*
3	1463	94.8	298	1	ADT2_HUMAN
4	1451	94.0	298	1	ADT2_RAT
5	1445	93.6	298	1	ADT2_MOUSE
6	1424	92.3	298	1	ADT1_RAT
7	1418	91.9	298	1	ADT1_MOUSE
8	1417	91.8	297	1	ADT1_BOVIN
9	1409	91.3	298	1	ADT1_HUMAN
10	1254.5	81.3	299	1	ADT1_DROME
11	1204	78.0	301	1	ADT1_ANOGA
12	978	63.4	339	1	ADT1_CHLKE
13	778.5	50.5	307	1	ADT3_YEAST*
14	772	50.0	308	1	ADT1_CHLRE
15	769	49.8	322	1	ADT1_SCHRO
16	768	49.8	322	1	ADT1_GOSHI
17	766	49.6	305	1	ADT1_NEUCR
18	762.5	49.4	303	1	ADT1_KLULA
19	760.5	49.3	318	1	ADT2_YEAST
20	750.5	48.6	385	1	ADT2_YEAST
21	750	48.6	387	1	ADT1_ARATH
22	748	48.5	386	1	ADT1_MAIZE
23	747	48.4	382	1	ADT1_SOLITU
24	744	48.2	387	1	ADT1_ORYZA
25	742.5	48.1	381	1	ADT1_MAIZE
26	740	48.0	331	1	ADT1_ARATH
27	739.5	47.9	331	1	ADT1_WHEAT
28	737.5	47.8	386	1	ADT2_SOLITU
29	727	47.8	309	1	ADT1_YEAST
30	305.5	19.8	331	1	ADT2_WHEAT
31	302	19.6	588	1	CMC3_CAEEL
32	300	19.4	588	1	CMC2_CAEEL
33	299	19.4	307	1	ODC2_BOVIN
					ODC2_YEAST

34	295	19.1	678	1	CMC1_HUMAN	075746 homo sapien
35	289.5	18.6	322	1	GDC_RAT	P16761 rattus norv
36	287.5	18.6	702	1	CMC1_CAEEL	Q21153 caenorhabd1
37	286	18.5	325	1	UCP5_HUMAN	095258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	0922b2 mus musculu
40	282.5	18.3	325	1	YEO8_SCHPO	013805 schizosacch
41	280	18.1	675	1	CMC2_HUMAN	Q9UJ50 homo sapien
42	272	17.6	315	1	MFT_HUMAN	Q9H2d1 homo sapien
43	270	17.5	315	1	SA18_HUMAN	Q9H1k4 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	Q9qxx4 mus musculu

ALIGNMENTS

RESULT 1
ADT3_HUMAN STANDARD; PRT; 298 AA.
ID ADT3_HUMAN
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE-89236396; PubMed-2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT ADP/ATP translocase.
RL J. Mol. Biol. 206:261-280(1989).
[2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mel G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RL Margolin J.F.;
RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA TISSUE-Brain, Cervix, Eye, and Lung;
RX MEDLINE-42388257; PubMed-1247932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow R.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fejtay J., Hailton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalka U., Smalls D.E.,
RA Sanchez A., Schein J.E., Jones S.D.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RP SEQUENCE OF 36-298 FROM N.A.
RN TISSUE-Liver;
RX MEDLINE-88124845; PubMed-2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

```

RT      Level In adult human liver.
CC      PRO. NAT. Acad. Sci. U.S.A. 85:377-381 (1988).
CC      CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC      MITOCHONDRIAL INNER MEMBRANE.
CC      -1- SUBUNIT: Homodimer.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein, Mitochondrial
CC      inner membrane.
CC      -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.lsb-ib.ch/announce/
CC      or send an email to license@lsb-ib.ch).
CC      -----
DR      EMBL: J03592; AAA36750.1; -
DR      EMBL: A007135; AAC01988.1; -
DR      EMBL: BC007295; AAH07293.1; -
DR      EMBL: BC007850; AAH07850.1; -
DR      EMBL: BC008737; AAH08737.1; -
DR      EMBL: BC008935; AAH08935.1; -
DR      EMBL: BC014775; AAH14775.1; -
DR      PIR: S03894; S03894.
DR      Genew; HGNC:10992; SLC25A6.
DR      MIM: 300151; -
DR      GO: GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
DR      GO: GO:0005471; F:ATP/ADP antiporter activity; NAS.
DR      GO: GO:0006854; P:ATP/ADP exchange; TAS.
DR      Interpro: IPR002067; Mlt_carrier.
DR      Interpro: IPR002030; Mlt_uncoupling.
DR      Interpro: IPR001993; Mitoch_carrier.
DR      Pfam: PF00153; mito_carri; 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
DR      KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW      Multigene family.
FT      TRANSMEM 12      29      1 (POTENTIAL).
FT      TRANSMEM 73      91      2 (POTENTIAL).
FT      TRANSMEM 117     134      3 (POTENTIAL).
FT      TRANSMEM 176     195      4 (POTENTIAL).
FT      TRANSMEM 214     231      5 (POTENTIAL).
FT      TRANSMEM 273     291      6 (POTENTIAL).
FT      REPEAT 1      100      1.
FT      REPEAT 101     208      2.
FT      REPEAT 209     298      3.
FT      REPEAT 305     408      4.
FT      CONFLICT 105     108      S -> F (IN REF. 3; AAH14775).
FT      CONFLICT 242     242      S -> F (IN REF. 3; AAH14775).
SQ      SEQUENCE 298 AA: 32866 MW: 1853459 F0E49672F CRG64;

Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3, 6e-128;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 MFEQAIISPAKFFLAGGIAAIAISKTVAAIEFEVKKLLLOVHASKQIADAKQYKIVDCTVR 60
Db 1 MFEQAIISPAKFFLAGGIAAIAISKTVAAIEFEVKKLLLOVHASKQIADAKQYKIVDCTVR 60
OY IPEEGGVISFPRKGLNAVIRYEPQTQALNFAKDKYKQIFIGVGDVHKTQFMFREFAGANLSS 120
Db 61 IPEEGGVISFPRKGLNAVIRYEPQTQALNFAKDKYKQIFIGVGDVHKTQFMFREFAGANLSS 120
OY IPEEGGVISFPRKGLNAVIRYEPQTQALNFAKDKYKQIFIGVGDVHKTQFMFREFAGANLSS 180
Db 61 IPEEGGVISFPRKGLNAVIRYEPQTQALNFAKDKYKQIFIGVGDVHKTQFMFREFAGANLSS 180
OY GAAGATSLCTFYPPDLPARTRLADVNGSGTEREERGLGDCGLVYIKRSGIRGLVQGSFVS 180
Db 121 GAAGATSLCTFYPPDLPARTRLADVNGSGTEREERGLGDCGLVYIKRSGIRGLVQGSFVS 180
OY VGGIITIRAAVFGYDTAKMLPDPKNTNHIYVSMNIAQVTVANAGVSYEPDTPRRBMM 240
Db 181 VGGIITIRAAVFGYDTAKMLPDPKNTNHIYVSMNIAQVTVANAGVSYEPDTPRRBMM 240
OY VGGIITIRAAVFGYDTAKMLPDPKNTNHIYVSMNIAQVTVANAGVSYEPDTPRRBMM 240
Db 181 VGGIITIRAAVFGYDTAKMLPDPKNTNHIYVSMNIAQVTVANAGVSYEPDTPRRBMM 240

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QY	DB	RESULT 2
		ID ADT3_BOVIN STANDARD: PRT: 298 AA.
		AC P32007;
		DT 01-JUL-1993 (Rel. 26, Created)
		DT 01-JUL-1993 (Rel. 26, Last sequence update)
		DT 16-OCT-2001 (Rel. 40, Last annotation update)
		DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).
		GN SLC25A6 OR ANT3.
		OS Bos taurus (Bovine).
		OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
		OX NCBI_TaxID=9913;
		XX [1]
		RP SEQUENCE FROM N.A.
		RX MEDLINE=89229093; PubMed=2540808;
		RA Powell S.J., Mead S.M., Runswick M.J., Walker J.E.;
		RT "How bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
		RL Biochemistry 28:866-873(1989).
		CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
		CC -1- SUBUNIT: Homodimer.
		CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
		CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
		CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
		CC -----
		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce , or send an email to license@isb-sib.ch).
		CC -----
		CC EMBL; M24103; AAA0769.1; -
		DR PIR; B43646; B43646.
		DR InterPro: IPR002067; Mit_carrier.
		DR InterPro: IPR002030; Mit_uncoupling.
		DR InterPro: IPR001993; Mitoch_carrier.
		DR Pfam; PF00153; mito_carr; 3.
		DR PRINTS: PR00926; MITOCARRIER.
		DR PRINTS: PR00784; MTUNCOUPLING.
		DR PROSITE: PS00215; MITOCH_CARRIER; 3.
		DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family.
		KM TRANSMEM 12 29 1 (POTENTIAL).
		FT TRANSMEM 72 91 2 (POTENTIAL).
		FT TRANSMEM 117 134 3 (POTENTIAL).
		FT TRANSMEM 176 195 4 (POTENTIAL).
		FT TRANSMEM 214 231 5 (POTENTIAL).
		FT TRANSMEM 273 291 6 (POTENTIAL).
		FT REPEAT 2 111 1.
		FT REPEAT 112 208 2.
		FT REPEAT 209 298 3.
		SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;
		Query Match 98.0%; Score 1512; DB 1; Length 298;
		Best Local Similarity 97.7%; Pred. No. 1.9e-15;
		Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0
0Y	1	MTBOAISEKPEFLAGGIAAISTAAPIERVKLLLOVQASQIADAKOYKGIYDCLR 60
	1	MTBOAISEKPEFLAGGIAAISTAAPIERVKLLLOVQASQIADAKOYKGIYDCLR 60
DB	1	MTBOAISEKPEFLAGGIAAISTAAPIERVKLLLOVQASQIADAKOYKGIYDCLR 60

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QY 61 IPKEGVLSFWKGNLANVIRYPTQALNFAKDKYQIFLGVGVDKHTQFMRYPAGNLAGS 120
DB 61 IPKEGVLSFWKGNLANVIRYPTQALNFAKDKYQIFLGVGVDKHTQFMRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVKTIRKSDIRGLYOGFNS 180
DB 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVKTIRKSDIRGLYOGFNS 180
QY 181 VOGIITIRAYFVYDTAKGMLDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRMM 240
DB 181 VOGIITIRAYFVYDTAKGMLDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRMM 240
QY 241 QSGRKADIMYGTVCWKRIFRDEGKAFKFGAMSNVLKMGCAFVLVLYDELKRYI 298
DB 241 QSGRKADIMYGTVCWKRIFRDEGKAFKFGAMSNVLKMGCAFVLVLYDELKRYI 298

RESULT 3
ADP2_HUMAN STANDARD; PRT; 298 AA.
ID ADP2_HUMAN. P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE-90375457; PubMed-2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence.
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-87166056; PubMed-3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagara J.A.,
RA Mazarella R.A., Schlessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozerzky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE-88124845; PubMed-2829183;
RA Houldsworth J., Attardi G.;
RT Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: M57424; AAA51737.1; -
DR EMBL: J02683; AAA35579.1; -
DR EMBL: I78810; AAB39266.1; -
DR EMBL: AC004000; AAB96547.1; -
DR EMBL: J03591; AAA36749.1; -
DR PIR: A29132; A29132.
DR Genew: HGNC:10991; SLC25A5.
DR MIM: 300150; -
DR GO: GO:0005887; C: Integral to plasma membrane; TAS.
DR GO: GO:0015207; F: adenine transporter activity; TAS.
DR GO: GO:0006832; P: small molecule transport; TAS.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carrier_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUOUCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; P973CAED92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;
Best Local Similarity 92.9%; Pred. No. 3, 8e-121;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDPLAGIAAIAISTAVAPIERVLLQVOHASKQIADKQYKGIYDCYR 60
DB 1 MTEQATSPAKDPLAGIAAIAISTAVAPIERVLLQVOHASKQIADKQYKGIYDCYR 60
QY 61 IPKEGVLSFWKGNLANVIRYPTQALNFAKDKYQIFLGVGVDKHTQFMRYPAGNLAGS 120
DB 61 IPKEGVLSFWKGNLANVIRYPTQALNFAKDKYQIFLGVGVDKHTQFMRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVKTIRKSDIRGLYOGFNS 180
DB 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGDGLVKTIRKSDIRGLYOGFNS 180
QY 181 VOGIITIRAYFVYDTAKGMLDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRMM 240
DB 181 VOGIITIRAYFVYDTAKGMLDPKNTHTIVSMIAQVTVTAAGVVSYPFDVRRMM 240
QY 241 QSGRKADIMYGTVCWKRIFRDEGKAFKFGAMSNVLKMGCAFVLVLYDELKRYI 296
DB 241 QSGRKADIMYGTVCWKRIFRDEGKAFKFGAMSNVLKMGCAFVLVLYDELKRYI 296

RESULT 4
ADP2_RAT STANDARD; PRT; 298 AA.
ID ADP2_RAT. P09073;
AC P09073;
DT 01-FEB-1995 (Rel. 31, Created)

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01-FEB-1995 (Rel. 31, last sequence update)
 16-OCT-2001 (Rel. 40, last annotation update)
 ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 (adenine nucleotide translocator 2) (ANT 2).
 DE SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamada M., Yamazaki N., Terada H.;
 RT Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.;
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 or send an email to license@isb-sib.ch).
 CC EMBL, D12771; BAA02238.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mltc_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;
 Query Match 94.08; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.98; Pred. No. 4 3e-120;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MPEQATSPKADPLAGLAAISTAYAPIERKLLQVQVHASKQIADKQYKIVCYR 60
 DB 1 MTDAAVSPKADPLAGLAAISTAYAPIERKLLQVQVHASKQIADKQYKIVCYR 60
 QY 61 IPEQGVLSFWKGNLANVIRFFPTQALNFAFDKTKQIFLGVDKHTQFWRIFAGNIASG 120
 DB 61 IPEQGVLSFWKGNLANVIRFFPTQALNFAFDKTKQIFLGVDKHTQFWRIFAGNIASG 120
 QY 121 GAAGATSLCFYVPLDFAFTRIAADVGSKTEFSGLDCLVTKTSKDGIRKGLYQGFVS 180
 DB 121 GAAGATSLCFYVPLDFAFTRIAADVGSKTEFSGLDCLVTKTSKDGIRKGLYQGFVS 180
 QY 181 VGGIITRYAAFGYVDKAKGLPDKNTHIVVSMIAQVTVAVAGVVSYPDITVRRMMK 240

181 VGGIITRYAAFGYVDKAKGLPDKNTHIVVSMIAQVTVAVAGVVSYPDITVRRMMK 240
 QY 241 QSGRKATDINTGTIDCWKRIARDEGSKAFKGSNVLRGSGAFVLYLDELTK 296
 DB 241 QSGRKATDINTGTIDCWKRIARDEGSKAFKGSNVLRGSGAFVLYLDELTK 296
 RESULT 5
 ID ADT2_MOUSE STANDARD; PRT: 298 AA.
 AC P51881; Q61311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 (adenine nucleotide translocator 2) (ANT 2).
 DE SLC25A5 OR ANT2.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudoautosomal genes and their mouse
 homologs.";
 RL Mamm. Genome 7:25-30(1996).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC TISSUE-Skeletal muscle;
 CC Sheldon J.G.;
 CC Thesis (1995), University of Cambridge, U.K.
 RN [3]
 RN SEQUENCE FROM N.A.
 RN STRAIN=C57BL/6;
 RC Costel P., Laplace C.;
 RA Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RL REVISIONS.
 RA Laplace C.;
 RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RN MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC EMBL, U27316; AAC52838.1; -
 DR EMBL, U10404; AAA19009.1; -
 DR EMBL, X70847; CAA50196.1; -
 DR EMBL, AF240003; AAF64471.1; -
 DR MGD; MG1:1353496; SLC25A5.
 DR InterPro: IPR002067; Mlt_carrier.

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DR InterPro: IPR002030; Mit. uncoupling.
DR InterPro: IPR001993; Mitoch. carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 93.6%; Score 1445; DB 1; Length 298;
Best Local Similarity 91.6%; Pred. No. 1,4e-119;
Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDFLAGGIAAISTAVAPIERVKLLQVQASAKQIADKQKIVDCIVR 60
DB 1 MDAAVSFADFLAGGAAISTAVAPIERVKLLQVQASAKQIADKQKIVDCIVR 60
QY 61 IPKEQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIASG 120
DB 61 IPKEQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSKGIRLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSKGIRLYOGFSVS 180
QY 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFDFVRRRMM 240
DB 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFDFVRRRMM 240
QY 241 QSGRKAGDIWYGTVDGWRKIFRDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296
DB 241 QSGRKAGDIWYGTVDGWRKIFRDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296
241 QSGRKAGDIWYGTVDGWRKIFRDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296

RESULT 6
ADT1_RAT STANDARD; PRT; 298 AA.
ID ADT1_RAT STANDARD; PRT; 298 AA.
AC 005962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-FEB-1994 (Rel. 28, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Blochum. Blochum. Acta 1152:192-196(1993)
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.

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CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X61667; CAA3842.1; -.
DR EMBL: D12770; BA02237.1; -.
DR F1R; I60173; I60173.
DR InterPro: IPR002067; Mit. carrier.
DR InterPro: IPR002030; Mit. uncoupling.
DR InterPro: IPR001993; Mitoch. carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1e-117;
Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQATSPAKDFLAGGIAAISTAVAPIERVKLLQVQASAKQIADKQKIVDCIVR 60
DB 1 MTEQATSPAKDFLAGGIAAISTAVAPIERVKLLQVQASAKQIADKQKIVDCIVR 60
QY 61 IPKEQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIASG 120
DB 61 IPKEQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSKGIRLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGSGTEREFGDGLVTKITSKGIRLYOGFSVS 180
QY 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFDFVRRRMM 240
DB 181 VQGIITRYRAVFGVYDTAKGMLDPKNTHTIVSMIAQVTVAVAGVSYFDFVRRRMM 240
QY 241 QSGRKAGDIWYGTVDGWRKIFRDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296
DB 241 QSGRKAGDIWYGTVDGWRKIFRDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296
241 QSGRKAGDIWYGTVDGWRKIFRDEGKAFKFGAMSVNLGMCAPVLYLYDELK 296

RESULT 7
ADT1_MOUSE STANDARD; PRT; 298 AA.
ID ADT1_MOUSE STANDARD; PRT; 298 AA.
AC P48962; 062164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MNC1).
GN SLC25A4 OR ANT1 OR ANCI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

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RN [1] SEQUENCE FROM N.A.
 RC STRAIN-07BL/6; TISSUE-Brain;
 RX MEDLINE-97059403; PubMed-8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA STRAIN-BALB/c; TISSUE-Muscle;
 RL Laplace C., Costet P.;
 RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RC SEQUENCE FROM N.A.
 RC MEDLINE-2388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeng B., Moore T., Max S.I., Wang J., Hatte N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hatte N.K.,
 RA Diatchenko L., Marusik K., Farmer A., Rubin G.M., Hong L.,
 RA Brabetz T.E., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M., Ustin T.B., Rosolyski S., Carroll P., Prange C.,
 RA Rana S.S., Louviano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bork S.A., McEwen P.J., McKernan K.J., Malek J.A., Cantarone P.H.,
 RA Villalón D., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RC [1-] FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC [1-] SUBUNIT: Homodimer.
 CC [1-] SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC [1-] DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC [1-] SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U27315; AAC52837.1; -;
 DR EMBL: X74510; CAA52616.1; -;
 DR EMBL: AF240002; AAF64470.1; -;
 DR EMBL: BC003791; AAH03791.1; -;
 DR EMBL: BC026925; AAH26925.1; -;
 DR PIR: S37210; S37210.
 DR MGI: MGI:1353495; Slc25a4.
 DR InterPro: IPR002067; Mtl_carrier.
 DR InterPro: IPR002030; Mtl_uncoupling.
 DR InterPro: IPR001993; Mtl_carrier.
 DR Pfam: PF00153; mtlcarr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 MW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 3 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 298 298 3.
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 FT SEQUENCE 298 AA: 32904 MW: 34849FEAD0981462 CRC64;
 Query Match 91.9%; Score 1418; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 3,4e-117;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MTEQAISFANDFLAGGIAAIAIKTAVAPIERVKLLQOVHASKQIADKQYKGIYDCTR 60
 DB 1 MGDAISFLKDFLAGGIAAIAVSKTAVAPIERVKLLQOVHASKQIADKQYKGIYDCTR 60
 QY 61 IPKRGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYAGNTLASG 120
 DB 61 IPKRGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYAGNTLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTPLADYVGSCTEREPGLDCLVYTKSDIRGLYGFSEVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTPLADYVGSCTEREPGLDCLVYTKSDIRGLYGFSEVS 180
 QY 121 VGGITIRAVFVYPTATGKMLPDKNTHIYVSMINQYTAAGVAVSPFTVRRMM 240
 DB 121 VGGITIRAVFVYPTATGKMLPDKNTHIYVSMINQYTAAGVAVSPFTVRRMM 240
 QY 241 OSGRKGDIVTYTCQWKRIFRDGKAFKGAWSNVLNGMGAGVLYVYDEIKKY 298
 DB 241 OSGRKGDIVTYTCQWKRIFRDGKAFKGAWSNVLNGMGAGVLYVYDEIKKY 298
 RESULT 8
 ADT1_BOVIN STANDARD; PRT: 297 AA.
 ID ADT1_BOVIN
 AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart isoform 71 (ADP/ATP translocase 1)
 DE (Adenine nucleotide translocator 1) (ANT 1).
 GN SLIC25A4 OR ANT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA MEDLINE-82188267; PubMed-2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
 RT differences in various tissues.";
 RL Biochemistry 28:866-873(1989).
 RN [2]
 RC SEQUENCE.
 RA MEDLINE-82188267; PubMed-7076130;
 RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
 RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
 RT mitochondria.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
 RN [3]
 RC SEQUENCE OF 207-297 FROM N.A.
 RA MEDLINE-86295775; PubMed-3017341;
 RA Rasmussen U.B., Wohlrab R.;
 RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

```

RT an unusually short 3'-noncoding sequence";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL: M13783; AAA30363.1; -.
DR EMBL: M24102; AAA30768.1; -.
DR PIR: A43646; XMO.
DR InterPro: IPR002067; Mt_carrier.
DR InterPro: IPR002030; Mt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MITOCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 91.8%; Score 1417; DB 1; Length 297;
Best Local Similarity 89.2%; Pred. No. 4.1e-117;
Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 2 TQGAISFAPDLAGGTAIAISKTAAPVIERVKLLLOVQASAKIOADKQKGIIVDCIVRI 61
DB 1 SDQALSFELDFLAGVAAISKTAAPVIERVKLLLOVQASAKIOADKQKGIIVDCIVRI 60
QY 62 PREQGLVSWFRGNLANVIRFPTQALNFAFKDKYKQIFGVDVKHFOFMRYFAGNLASGG 121
DB 61 PREQGLVSWFRGNLANVIRFPTQALNFAFKDKYKQIFGVDVKHFOFMRYFAGNLASGG 120
QY 122 AAGASLSCVYVPLDFARTRIADVSGSGTEREFGIGDCLVTKTSKDGKIGLQGSVSY 181
DB 121 AAGASLSCVYVPLDFARTRIADVSGSGTEREFGIGDCLVTKTSKDGKIGLQGSVSY 180
QY 182 OGIIIRAAVFGYVDVDAKGMGLPDKRTHIVVSMNIQOTYAVAGVSYSPEDYVRRRMMQ 241
DB 181 OGIIIRAAVFGYVDVDAKGMGLPDKRTHIVVSMNIQOTYAVAGVSYSPEDYVRRRMMQ 240
QY 242 SGRKAGDINTYGTGVDCKRIKIFRDEGKAEFFKGAMSVNLKMGGAFLVLYDELKRYI 298
DB 241 SGRKAGDINTYGTGVDCKRIKIFRDEGKAEFFKGAMSVNLKMGGAFLVLYDELKRYI 297

RESULT 9
ADT1_HUMAN STANDARD; PRT; 298 AA.
AC P12235;

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DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Meekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed.";
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant P.L., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smolins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-37 FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houlsworth J., Attardi G.;
RT Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [6]
RP VARIANTS PRO-114 AND MET-289.
RX MEDLINE=20385067; PubMed=10926541;
RA Kaukonen J., Jusellius J.K., Tienari V., Kytala A., Zeviani M.,
RA Comi G.P., Keranen J., Peltonen L., Sommalainen A.;
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

```

CC MITOCHONDRIAL INNER MEMBRANE

CC -1- SUBUNIT: Homodimer.

CC -1- SUBUNITAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC

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CC

CC EMBL: J02966; AAA61223.1; -

CC EMBL: J03593; AAA61223.1; -

CC EMBL: J04982; AAA51736.1; -

CC EMBL: BC008664; AAH08664.1; -

CC PIR: A44778; A44778.

CC GeneW: HGNC:10990; SLC25A4.

CC MIM: 103220; -

CC MIM: 157640; -

CC GO: GO:0005887; C:Integral to plasma membrane; TAS.

CC GO: GO:0005739; C:mitochondrion; TAS.

CC GO: GO:0015207; F:adenine transporter activity; TAS.

CC GO: GO:0006093; F:energy pathway; TAS.

CC GO: GO:0006093; F:mitochondrial genome maintenance; TAS.

CC GO: GO:0006833; P:small molecule transport; TAS.

CC InterPro: IPR002067; MLC_carrier.

CC InterPro: IPR002030; MLC_uncoupling.

CC InterPro: IPR001993; Mitoch_carrier.

CC Pfam: PF00153; mito_carr_3

CC PRINTS: PR00926; MITOCARRIER.

CC PRINTS: PR00784; MTUNCOUPLING.

CC PROSITE: PS00215; MITOCH_CARRIER_3.

CC KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multi-pass family; Disease mutation.

CC KW

CC FT TRANSMEM 12 29 1 (POTENTIAL).

CC FT TRANSMEM 7 31 2 (POTENTIAL).

CC FT TRANSMEM 117 134 3 (POTENTIAL).

CC FT TRANSMEM 176 195 4 (POTENTIAL).

CC FT TRANSMEM 214 231 5 (POTENTIAL).

CC FT TRANSMEM 273 291 6 (POTENTIAL).

CC FT REPEAT 1 110 1.

CC FT REPEAT 111 208 2.

CC FT REPEAT 209 298 3.

CC FT VARIANT 114 114 1.

CC FT VARIANT 289 289 1.

CC FT CONFLICT 16 16 1 (IN PEO).

CC FT CONFLICT 147 149 1 (IN PEO).

CC FT CONFLICT 227 227 1 (IN REF. 3).

CC FT CONFLICT 227 227 1 (IN REF. 3).

CC SEQUENCE 298 AA; 33064 MW; 59F0DFAEAC4E7CBB CRC64;

Query Match Best Local Similarity 91.3%; Score 1409; DB 1; Length 298; Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQAIQFAKQDFLAGIQAIAIKTNVAPIRKVLQLQVQVHASKQIADKQKIGVDCIYR 60

DB 1 MGDHAWSEFLDPLAGVAAVAASKTAVAPIRSVKLLQVQVHASKQISAEKQKGIIDCVYR 60

QY 61 IPKQGVLSFWKGNLANVIRPPTQALNFAPKDKYKQIFLGVDKHNQFMYRAGNIALSG 120

DB 61 IPKQGVLSFWKGNLANVIRPPTQALNFAPKDKYKQIFLGVDKHNQFMYRAGNIALSG 120

QY	123	GAAGATGTCSCFEYYPDEAFRRFLADYVKGSGTGERRGRGDCLVITITSDGIRLQYGFESV	160
Db	121	GAAGATGTCSCFEYYPDEAFRRFLADYVKGSGTGERRGRGDCLVITITSDGIRLQYGFESV	160
QY	181	VGGIITTYAAAFEGYVYDPAAGMLPDPKRNTHIVSMNIAOTATYANAGVSVPEPTVARRBM	240
Db	181	VGGIITTYAAAFEGYVYDPAAGMLPDPKRNTHIVSMNIAOTATYANAGVSVPEPTVARRBM	240
QY	241	OSGRGAGDIATGTCYVOCMRIRTRDSCGAFKRCAGSWLVLMGAGAVLVLDLKKYI	298
Db	241	OSGRGAGDIATGTCYVOCMRIRTRDSCGAFKRCAGSWLVLMGAGAVLVLDLKKYI	298
RESULT 10			
ADT_DROME			
ADT_DROME	STANDARD;	PTT;	299 AA.
AC	Q26365;	P91614;	Q26254;
ADT	15-JUL-1998	(Rel. 36, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DE	15-SEP-2003	(Rel. 42, Last annotation update)	
DE	ADP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT) (Stress sensitive B protein).		
GN	GENB OR A/A-T OR CG16944.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
OC	NBL_TaxID=7227;		
PN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE-92389367;		
RA	Leuvi A., Tselicou S.G.;		
RT	A cDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases.		
RL	J. Mol. Evol. 35:14-50(1992).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-94350065;		
RA	Georgie R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champé M., Pfeiffer B.D., Men K.H., Doyle K., Baxter E.G., Helt G., Nelson C., Miklos G.L.G., Abrial J.F., Abghyani A., An H.-J., Andrews-Pfannkuch C., Baldwin D., Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borokova D., Busam M.R., Bouck J., Brockstein P., Bröttler P., Burris K.C., Butman D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P., de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Bletz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferrelle S., Fleischmann W., Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K., Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwu C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kension J.A., Ketchum K.A.,		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;		
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Berkeley;		
RC	ADAMS-20196006;		
RC	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-Oregon-R;		
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburn		

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Meriklov G., Mishina N.V., Modarri C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muray D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Slden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wastaman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).

RN [5]
 RP SEQUENCE FROM N.A.

RC STRAIN-Berkeley; TISSUE-Larva, Ovary, and Pupa;

RX MEDLINE-22426066; PubMed-12537569;

RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Garin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Ceiniker S.E.;

RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).

CC -1- DOMAIN: Composed of three homologous domains.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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DR EMBL: S43651; AAB23114.1; -;
 DR EMBL: S71762; AAB31734.3; -;
 DR EMBL: Y10618; CAAT1628.1; -;
 DR EMBL: AEO03484; AAF47957.1; -;
 DR EMBL: AY060978; AAL28526.1; -;
 DR EMBL: AY070894; AAL48516.1; -;
 DR Flybase: FBgn0003360; sepb.
 DR GO: GO:0005743; C:mitochondrial inner membrane; IEP.
 DR GO: GO:0006839; P:mitochondrial transport; IMP.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mltch_carrier.
 DR Pfam: PF00153; mltch_carrier_2.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR TrEMBL: L11617; AAB04105.1; -;
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 215 232 5 (POTENTIAL).
 FT TRANSMEM 274 292 6 (POTENTIAL).
 FT TRANSMEM 18 19 GI -> OV (IN REF. 1 AND 2).
 FT TRANSMEM 81 81 I -> Y (IN REF. 1).
 FT TRANSMEM 201 201 MISSING (IN REF. 1 AND 2).
 FT TRANSMEM 267 267 G -> A (IN REF. 2).
 FT TRANSMEM 268 269 TG -> P (IN REF. 1 AND 2).
 FT TRANSMEM 270 270 A -> S (IN REF. 1).
 FT TRANSMEM 270 270 A -> C (IN REF. 2).
 FT TRANSMEM 299 AA; 32909 MM; D51F3E2A70BD5B8 CRC64;
 SQ SEQUENCE

Query Match 81.3%; Score 1254.5; DB 1; Length 299;
 Best Local Similarity 80.6%; Pred. No. 7.5e-103;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 QY 5 AISEAADFLAGGIAAISTAVPIRVLVLQVQASQIADAKRYKIVCIYPIRE 64
 DB 7 AGEVAFDFAAGGISAASVSTAAPIERVKLLQVQHSIKQISPDQKQKMWDFIRPE 66
 QY 65 OGCLSEWRNLAVNIYRFTQALNFAFKRYKQIFGVDKHPQFRYAGNLASGAAG 124
 DB 67 QGSSSWRNLAVNIYRFTQALNFAFKRYKQIFGVDKHPQFRYAGNLASGAAG 126
 QY 125 AHSCLFVPLDEARFIADAVGKSTEREFGIDCLVITRSDGIRGLYQGFVSVOGI 184
 DB 127 ATSLCEVPLDEARFIADAVGKSTEREFGIDCLVITRSDGIRGLYQGFVSVOGI 185
 QY 185 IIRYAFVGYVDPAKMLDPPKNTPIYISWALQVTVAGIVSYFPDVRMMQSGR 244
 DB 186 IIRYAFVGYVDPAKMLDPPKNTPIYISWALQVTVAGIVSYFPDVRMMQSGR 245
 QY 245 KGADIMYTGTVDCWRKIFRDEGKAFKAGMSVNLKMGAFVLVYDELKVI 298
 DB 246 KATEVYKNTLHGMATIANQEGTGAFFKAFSNIILGTGAFVLVYDELKVI 299

RESULT 11
 ID ADT_ANOGA STANDARD; PRT; 301 AA.
 AC 027238;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide
 DE translocator) (ANT).
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-G3;
 RX MEDLINE-94348635; PubMed-8069414;
 RA Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;
 RT "A cDNA encoding an ADP/ATP carrier from the mosquito *Anopheles*
 RT *gambiae*.";
 RL Insect Mol. Biol. 3:35-40(1994).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9FDA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;
 Best Local Similarity 77.7%; Pred. No. 2, 1e-98;
 Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

OY 1 MFPOA--ISFADPFLAGIAAISKTAAPTEIEVKLLLOVQASQIAADKQYGYIDTC 58
 DB 1 MTRKADPYGFADFLAGISAAVSKTAVAPIERVKLLLOVQASQIAADKQYGYIDTC 60
 OY 59 VRIPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKOIFLGVGDKHTOPMRYFAGNTA 118
 DB 61 VRIPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKOIFLGVGDKHTOPMRYFAGNTA 120
 OY 119 SGGAAGATSLCEVYPLDFARTRLADYKSGTEREFRLGDCLVKTKSDGIRGLYGFES 178
 DB 121 SGGAAGATSLCEVYPLDFARTRLADYKSGTEREFRLGDCLVKTKSDGIRGLYGFES 180
 OY 179 VSVQGIIRAYAFEGVYDFAKGMLDPKNTIIVYSMMIQVTAVAGVSYPEPTVRRRM 238
 DB 181 VSVQGIIRAYAFEGVYDFAKGMLDPKNTIIVYSMMIQVTAVAGVSYPEPTVRRRM 240
 OY 239 MMSGHRGADIMYTGVCNMRKIFRDGKAFKAGMSNVLRKMGAFVLYDELKRYV 298
 DB 241 MMSGHRGADIMYTGVCNMRKIFRDGKAFKAGMSNVLRKMGAFVLYDELKRYV 300

RESULT 12
 ID ADT_CHLKE STANDARD; PRT; 339 AA.

AC P31692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 OS Chlorella kessleri.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorellia.
 OX NCBI_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92084708; PubMed=1748677;
 RA Hilgath C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella."; J. Biol. Chem. 266:24044-24047(1991).
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 CC EMBL: M76669; AAA33027.1; -
 CC DR PIR: A41677; A41677.
 CC DR Interpro: IPR002067; Mit_Carrier.
 CC DR Interpro: IPR001993; Mitoch_carrier.
 CC DR Pfam: PF00153; mito_carr; 3.
 CC DR PRINTS: PR00926; MITOCHARRIER.
 CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A3B3942 CRC64;

Query Match 63.4%; Score 978; DB 1; Length 339;
 Best Local Similarity 66.9%; Pred. No. 1, 6e-78;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

OY 6 ISFADPFLAGIAAISKTAAPTEIEVKLLLOVQASQIAADK--QYKGIYDCIYRIPK 63
 DB 39 MAFVRLDLAGTAGAISKTAAPTEIEVKLLLOVQASQIAADKQYGYIDTC 98
 OY 64 EGVLSFMRGNLANVIRYPTQALNFAFKDKYKOIFLGVGDKHTOPMRYFAGNTA 123
 DB 99 EGVLSFMRGNLANVIRYPTQALNFAFKDKYKOIFLGVGDKHTOPMRYFAGNTA 157
 OY 124 GATSLCEVYPLDFARTRLADYKSGTEREFRLGDCLVKTKSDGIRGLYGFES 183
 DB 158 GATSLCEVYPLDFARTRLADYKSGTEREFRLGDCLVKTKSDGIRGLYGFES 216
 OY 184 IIVYRAVFGVYDFAKGMLDPKNTIIVYSMMIQVTAVAGVSYPEPTVRRRM 242
 DB 217 IIVYRAVFGVYDFAKGMLDPKNTIIVYSMMIQVTAVAGVSYPEPTVRRRM 276
 OY 243 GHRGADIMYTGVCNMRKIFRDGKAFKAGMSNVLRKMGAFVLYDELKRYV 298
 DB 277 ---GGEROYNGTIDCMRKVAQCEKMAFFKAGMSNVLRKMGAFVLYDELKRYV 329

RESULT 13
 ID ADT_YEAST STANDARD; PRT; 307 AA.

AC P18238;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP/ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).
 GN AAC3 OR YBR085W OR YBR0753.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90324269; PubMed=2165073;
 RA Kolarov J., Kolarova N., Nelson N.;
 RT "A third ADP/ATP translocator gene in yeast."; J. Biol. Chem. 265:12711-12716(1990).
 RL J. Biol. Chem. 265:12711-12716(1990).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=S288C;
 CC Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestazu A., Vissers S.;
 CC Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC SEQUENCE OF 38-307 FROM N.A.
 CC STRAIN=S288C;
 CC Feldmann H., Manhaupt G., Schwarzlose C., Vetter I.;
 CC Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----

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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:08:37 ; Search time 97 Seconds

(without alignments)
792.780 Million cell updates/sec

Title: US-09-811-094-33

Sequence: 1 MTEQAIISFAKDFLAGGIAAA.....LRGCGAYVLYLDELKVI 298

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

830525

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_UMBIC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1474	95.5	298	13	OBAYM3	OBAYM3 gallus gall
2	1451	94.0	298	6	OBSCOH5	OBSCOH5 bos taurus
3	1446	93.7	298	13	OBTH10	OBTH10 brachydantio
4	1422	92.2	298	6	O46373	O46373 oryctolagus
5	1421	92.1	298	13	O919M9	O919M9 xenopus lae
6	1414	91.6	298	11	OBHV19	OBHV19 mus musculu
7	1409	91.3	298	13	O9PRH1	O9PRH1 rana rugosa
8	1406	91.1	298	13	O9PRH2	O9PRH2 rana rugosa
9	1402	90.9	298	13	O9YIC4	O9YIC4 rana rugosa
10	1300	84.3	299	5	O95VX4	O95VX4 etimostigm
11	1259	81.6	317	13	O91336	O91336 rana sylvat
12	1254.5	80.1	312	5	O8IRAO	O8IRAO drosophila
13	1235.5	80.3	300	5	O9NHM5	O9NHM5 lucilia cup
14	1187.5	77.0	288	5	O44093	O44093 drosophila
15	1183.5	76.7	288	5	O44094	O44094 drosophila
16	1176.5	76.2	304	5	O25129	O25129 halocynthia

17	1159	75.1	254	11	O8BK05	O8BK05 mus musculu
18	1137.5	73.7	307	5	O62526	O62526 drosophila
19	1119	72.5	315	4	O9HOC2	O9HOC2 homo sapien
20	1041	67.5	313	5	O21103	O21103 caenorhabd1
21	1039	67.3	313	5	P91410	P91410 caenorhabd1
22	1038	67.3	300	5	O45865	O45865 caenorhabd1
23	1036.5	67.2	310	10	O8H727	O8H727 phytothor
24	996	64.5	309	5	O97470	O97470 dictyostel1
25	993.5	64.4	300	5	O01813	O01813 caenorhabd1
26	993	64.4	300	5	O17407	O17407 caenorhabd1
27	973.5	63.1	318	5	O9BJ36	O9BJ36 toxoplasma
28	947	61.4	301	5	O8IT34	O8IT34 plasmodium
29	946.5	61.3	307	8	O9XM22	O9XM22 ascaris sun
30	944	61.2	301	5	O25692	O25692 plasmodium
31	943	61.1	301	5	O8MYR4	O8MYR4 euplotus sp
32	943	60.7	305	5	O8MYR7	O8MYR7 plasmodium
33	936	60.4	308	5	O8MYR8	O8MYR8 nyctotherus
34	932	60.4	308	5	O8MYR5	O8MYR5 nyctotherus
35	924	59.9	306	5	O8MYR6	O8MYR6 nyctotherus
36	924	59.9	308	5	O9X659	O9X659 sus scrofa
37	827	53.6	170	6	O9P8M1	O9P8M1 yarrowia 11
38	778.5	50.5	305	3	O8JOM2	O8JOM2 yarrowia 11
39	767.5	49.7	302	3	P91270	P91270 caenorhabd1
40	764	49.5	326	5	O76286	O76286 trypanosoma
41	760	49.3	307	5	O74260	O74260 candida par
42	759	49.2	303	3	O18683	O18683 caenorhabd1
43	756.5	49.0	306	5	O26697	O26697 trypanosoma
44	753	48.8	307	5	O8JOU1	O8JOU1 gaemannomy
45	749	48.5	315	3		

ALIGNMENTS

RESULT 1

ID	OBAYM3	PRELIMINARY	PRT	298 AA.
AC	OBAYM3			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	ATP/ADP antiporter.			
GN	AVANT.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;			
RT	"Cold-induced mitochondrial uncoupling and expression of chicken UCP			
RT	and ANT mRNA in chicken skeletal muscle.";			
RL	FEBS Lett. 0:0-0(2002).			
DR	EMBL; AB088686; BAC1533.1; -			
SQ	SEQUENCE 298 AA; 32847 MW; 1174CSECA400A10D CRC64;			
Query Match	95.5%	Score 1474;	DB 13;	Length 298;
Best Local Similarity	93.08;	Pred. No. 2.5e-125;		
Matches 277;	Conservative 14;	Mismatches 7;	Indels 0;	Gaps 0;
OY	1 MTEQAIISFAKDFLAGGIAAAISKTAAPIERVVLLIQVOHASKOIADROKYGIVDCIYR 60			
DB	1 MDAQISFLKDFLAGGVAAAIKSTNAPIERVRLILQVOHASQIADROKGIIDCYVR 60			
OY	61 IPEQGVLSFWKGNLANVIRFPTQALNFAFDKVKQIFLGVDKRTQWRFPAGWLASG 120			
DB	61 IPEQGVLSFWKGNLANVIRFPTQALNFAFDKVKQIFLGVDKRTQWRFPAGWLASG 120			
OY	121 GAAGATSLCFVYPLDFAPTRILADVGKSGEREFRGLGCLVYITRSDGIRIGYOGFSYS 180			
DB	121 GAAGATSLCFVYPLDFAPTRILADVGKAGADREFSLGCLVYITRSDGIRIGYOGFSYS 180			

[illegible]

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RESULT 2
08SQHS
ID 08SQHS; PRELIMINARY; PRT; 298 AA.
AC 08SQHS;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RA Yasuaki N., Shiohara Y., Tanida K., Terada H.;
RT Structural properties of mammalian mitochondrial ADP/ATP carriers
RT identified from the isoforms *;
RT differences in the isoforms *;
NC MitoChondr1.1.371-379(2002).
DR EMBL:AB054533; GAB84671;
DR InterPro:IPR001993; Mitoc;
DR Pfam:PF00153; mito_car; 3_carrier.
DR PROSITE:PS00215; MITOC_CARRIER_3
SQ SEQUENCE 298 AA; 32955 MW; CB6897B987B79C0 CRC64;

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Query Match	94.0%;	Score 1451;	DB 6;	Length 298;
Best Local Similarity	92.2%;	Pred. No. 3e-123;		
Matches 273; Conservative	13;	Mismatches 10;	Indels 0;	Gaps 0;

[illegible]

	RESULT 3
OBJH10	
ID	OBJH10
AC	OBJH10
OBJH10:	PRELIMINARY; PRT; 298 AA.
DT	01-OCT-2002 (TREMBLrel, 22, Created)
DT	01-OCT-2002 (TREMBLrel, 22, last sequence update)
DT	01-MAR-2003 (TREMBLrel, 23, last annotation update)
DE	Solute carrier family 25 member 5 protein.
GN	SLC25A5.
OS	Brechiydanio rerio (zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.

Query Match	93.7%	Score 1446	DB 13	Length 298
Best Local Similarity	91.9%	Pred. No. 8	Se-123	
Matches 2/4	Conservative 15	Mismatches 9	Indels 0	Gaps 0

[illegible]

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RESULT 4
ID 046373
AC 046373 PRELIMINARY; PRT; 298 AA.
AD 046373;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RA Yamauchi N., Kasai M.;
RL "Identification of a 30kDa calsequestrin-binding protein, which
RT regulates calcium release from sarcoplasmic reticulum of rabbit
RT skeletal muscle."
RL J. Biochem. 335:541-547(1998).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB009386; BA227277.1; -
DR InterPro; IPR001993; Mitoc_carr1.
DR InterPro; IPR002067; Mit_carr1.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; Mitc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.

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DR PROSITE: PS00215; MITOCH_CARRIER: 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;
Query Match 92.2%; Score 1422; DB 6; Length 298;
Best Local Similarity 88.9%; Pred. No. 1.3e-120;
Matches 269; Conservative 20; Mismatches 13; Indels 0; Gaps 0;
QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
DB 1 MSQALSLFKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
QY 61 IPKEQGLSWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEQGLSWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDCLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDCLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSWMTAQVTAVAGVSYFPDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSWMTAQVTAVAGVSYFPDVRRRMM 240
QY 241 QSGRKADIMYTGTVOCWKRIFFDEGKAFKFGAMSNVLRGMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVOCWKRIADDEGAKAFKFGAMSNVLRGMGAFVLYLDELKRYI 298
RESULT 5
Q919M9 PRELIMINARY; PRT; 298 AA.
AC Q919M9; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC NCBL_TaxID=8355; Xenopus.
RN NCBL_TaxID=8355;
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
Dynamic Patterns of Expression During Development.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF231347; AAF63471.1; -
DR Interpro: IPR001993; Mitoch_carrier.
DR Interpro: IPR002067; Mit_carrier.
DR Interpro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carrier_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
Query Match 92.1%; Score 1421; DB 13; Length 298;
Best Local Similarity 90.3%; Pred. No. 1.6e-120;
Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
QY 61 IPKEQGLSWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEQGLSWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDCLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDCLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSWMTAQVTAVAGVSYFPDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSWMTAQVTAVAGVSYFPDVRRRMM 240
QY 241 QSGRKADIMYTGTVOCWKRIFFDEGKAFKFGAMSNVLRGMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVOCWKRIADDEGAKAFKFGAMSNVLRGMGAFVLYLDELKRYI 298
RESULT 6
Q8BVT9 PRELIMINARY; PRT; 298 AA.
AC Q8BVT9; 08BVT9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK078077; BAC37117.1; -
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;
Query Match 91.6%; Score 1414; DB 11; Length 298;
Best Local Similarity 88.6%; Pred. No. 6.8e-120;
Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;
QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIVDCIVR 60
QY 61 IPKEQGLSWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
DB 61 IPKEQGLSWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTHQFRYAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDCLVITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRRLADVGKSGTEREFGIDCLVITKSDGIRGLYOGFSVS 180
QY 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSWMTAQVTAVAGVSYFPDVRRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKMLDPKNTHTIVSWMTAQVTAVAGVSYFPDVRRRMM 240
QY 241 QSGRKADIMYTGTVOCWKRIFFDEGKAFKFGAMSNVLRGMGAFVLYLDELKRYI 298
DB 241 QSGRKADIMYTGTVOCWKRIADDEGAKAFKFGAMSNVLRGMGAFVLYLDELKRYI 298
RESULT 7
Q9PRH1 PRELIMINARY; PRT; 298 AA.
AC Q9PRH1; 09PRH1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=8410;
 (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99083429; PubMed-9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of
 z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB0084463; BAA36513.1; -;
 DR EMBL: AB0084464; BAA36510.1; -;
 DR EMBL: AB0084465; BAA36511.1; -;
 DR EMBL: AB0084462; BAA36512.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 DR Membrane: Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33054 MW; B0E23AD56F54BD36 CRC64;
 SQ
 Query Match 91.3%; Score 1409; DB 13; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1,9e-119;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 OY 1 MTEQAISPAKDFLAGGTAIAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIYR 60
 DB 1 MTDAAISPAKDFLAGGTAIAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIYR 60
 OY 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKQKIFLGVGDKHGFQFRRYFAGNLASG 120
 DB 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKQKIFLGVGDKHGFQFRRYFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLDCLVTKNSDGIKGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLDCLVTKNSDGIKGLYQGFVS 180
 OY 181 VOGIIRAAVFGVYDITAKGMLDPKNTHTVSMIAQVTVAVAGVSYPPDVTYRRRMM 240
 DB 181 VOGIIRAAVFGVYDITAKGMLDPKNTHTVSMIAQVTVAVAGVSYPPDVTYRRRMM 240
 OY 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 DB 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 OY 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 DB 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 RESULT 8
 OYPRH2 PRELIMINARY; PRT: 298 AA.
 AC OYPRH2: (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Winkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99083429; PubMed-9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of
 z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB0084460; BAA36510.1; -;
 DR EMBL: AB0084458; BAA36508.1; -;
 DR EMBL: AB0084459; BAA36509.1; -;

DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 DR Membrane: Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33062 MW; B0E225E67599A06 CRC64;
 SQ
 Query Match 91.1%; Score 1406; DB 13; Length 298;
 Best Local Similarity 88.3%; Pred. No. 3.6e-119;
 Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
 OY 1 MTEQAISPAKDFLAGGTAIAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIYR 60
 DB 1 MTDAAISPAKDFLAGGTAIAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIYR 60
 OY 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKQKIFLGVGDKHGFQFRRYFAGNLASG 120
 DB 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKQKIFLGVGDKHGFQFRRYFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLDCLVTKNSDGIKGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLDCLVTKNSDGIKGLYQGFVS 180
 OY 181 VOGIIRAAVFGVYDITAKGMLDPKNTHTVSMIAQVTVAVAGVSYPPDVTYRRRMM 240
 DB 181 VOGIIRAAVFGVYDITAKGMLDPKNTHTVSMIAQVTVAVAGVSYPPDVTYRRRMM 240
 OY 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 DB 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 OY 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 DB 241 OSGRKGAIDVYTGVCWKRIKFRDEGKAFKFGAMSNVLRGKGAFAVLVLYDELKRYI 298
 RESULT 9
 OYPRH2 PRELIMINARY; PRT: 298 AA.
 AC OYPRH2: (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
 DT 01-MAY-2003 (Tremblrel. 10, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Winkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99083429; PubMed-9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of
 z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB0084457; BAA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 DR Membrane: Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
 SQ
 Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 8.3e-119;
 Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 OY 1 MTEQAISPAKDFLAGGTAIAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIYR 60
 DB 1 MTDAAISPAKDFLAGGTAIAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIYR 60

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Db      1 MTDAAISFAKDFLAGGAAAIKSTAVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
QY      61 IPKEGVSLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYFAGNLASG 120
        ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKEGVSLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYFAGNLASG 120
QY      121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKSDGIRGLYOGFSVS 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKSDGIRGLYOGFSVS 180
QY      181 VOGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMTIAQVTVAVAGVSYFPDVRRRMM 240
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMTIAQVTVAVAGVSYFPDVRRRMM 240
QY      241 QSGRKADIMYTGTVDCWKRIFFDEGKAFKFGAMSVNLKMGCAFVLVLYDELKRYI 298
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKAEIMYSTIDCKMKIARDEGSRAPFKGAMSVNLKMGCAFVLVLYDELKRYI 298

RESULT 10
Q95VX4 PRELIMINARY; PRT; 299 AA.
AC      095VX4;
AT      01-DEC-2001 (Tremblrel. 19, Created)
DT      01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE      01-MAR-2003 (Tremblrel. 23, Last annotation update)
OS      Ethmostigmus rubripes.
OC      Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC      Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX      NCBI_TaxID=62613;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Burnell J.N.;
RT      "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT      rubripes."
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF401558; AAL02100.1;
DR      InterPro: IPR001993; Mitoch_carrier.
DR      InterPro: IPR002067; Mlt_carrier.
DR      Pfam: PF00153; mltoc_carri; 3.
DR      PRINTS: PR00926; MITOCH_CARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER.
SQ      SEQUENCE. 299 AA; 33037 MW; 3C3B8CB26E7C3C5E CRC64;

Query Match      84.3%; Score 1300; DB 5; Length 299;
Best Local Similarity 81.5%; Pred. No. 1.5e-109;
Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;
QY      1 MTEQAISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIDCTVR 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MTDAAISFAKDFLAGGAAAIKSTAVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
QY      61 IPKEGVSLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYFAGNLASG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKEGVSLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYFAGNLASG 120
QY      121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKSDGIRGLYOGFSVS 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKSDGIRGLYOGFSVS 180
QY      181 VOGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMTIAQVTVAVAGVSYFPDVRRRMM 240
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMTIAQVTVAVAGVSYFPDVRRRMM 240
QY      241 QSGRKADIMYTGTVDCWKRIFFDEGKAFKFGAMSVNLKMGCAFVLVLYDELKRYI 298
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKADIMYTGTVDCWKRIFFDEGKAFKFGAMSVNLKMGCAFVLVLYDELKRYI 298

RESULT 11
Q91336 PRELIMINARY; PRT; 317 AA.

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AC      Q91336;
DT      01-NOV-1996 (Tremblrel. 01, Created)
DT      01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE      ADP/ATP translocase.
OS      Rana sylvatica (Wood frog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX      NCBI_TaxID=45438;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tissue-Liver;
RC      TISSUE=Liver;
RX      MEDLINE=97398141; Pubmed=9256066;
RA      Cai Q., Greenway S.C., Storey K.B.;
RT      "Differential regulation of the mitochondrial ADP/ATP translocase gene
RT      in wood frogs under freezing stress."
RL      Biochim. Biophys. Acta 1353:69-78(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Tissue-Liver;
RC      TISSUE=Liver;
RA      Cai Q., Storey K.B.;
RL      Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL: U44832; AAA97882.2;
DR      InterPro: IPR001993; Mitoch_carrier.
DR      InterPro: IPR002067; Mlt_carrier.
DR      Pfam: PF00153; mltoc_carri; 3.
DR      PRINTS: PR00926; MITOCH_CARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER.
KW      Membrane; Transmembrane; Transport.
SQ      SEQUENCE. 317 AA; 35005 MW; 5F6657ED8D5CEB72 CRC64;

Query Match      81.6%; Score 1259; DB 13; Length 317;
Best Local Similarity 86.8%; Pred. No. 8.2e-106;
Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
QY      1 MTEQAISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADKQKGIIDCTVR 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MTDAAISFAKDFLAGGAAAIKSTAVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
QY      61 IPKEGVSLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYFAGNLASG 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKEGVSLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYFAGNLASG 120
QY      121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKSDGIRGLYOGFSVS 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKSDGIRGLYOGFSVS 180
QY      181 VOGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMTIAQVTVAVAGVSYFPDVRRRMM 240
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMTIAQVTVAVAGVSYFPDVRRRMM 240
QY      241 QSGRKADIMYTGTVDCWKRIFFDEGKAFK 272
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKAEIMYSTIDCKMKIARDEGSRAPFR 272

RESULT 12
Q81RAO PRELIMINARY; PRT; 312 AA.
AC      Q81RAO;
AT      01-MAR-2003 (Tremblrel. 23, Created)
DT      01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE      01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE      CG16944-PC.
GN      SESB.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.

```

RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abrell J.F., Abmayant A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck P., Brokstein P., Brotler P.,
 RA Burley K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fierman C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glisick A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Lavitsky A.A., Li J., Li B., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.E., McPherson D.,
 RA Markovlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler M.P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spiedling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu Q., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amandides P.G., Brandon R.C., Rogers Y.,
 RA Barton J.A., An H., Baldwin D., Barton J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K.J., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,
 RA Ferreira S., Flise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Pacled J.M., Part S., Patel S., Pfeiffer B., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Sytkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RA "Sequencing of *Drosophila melanogaster* genome.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Hang Y., Kaminker J.S., Prochnick S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Clump M., Drysdale R., Emmert D., Flise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RA "Annotation of *Drosophila melanogaster* genome.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.

RA FlyBase:
 RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003484; AAN09267.1; -
 SEQUENCE 312 AA: 34214 MW: 7805634E/4E168DF CRC64;
 SQ
 Query Match 81.3% Score 1254.5; DB 5; Length 312;
 Best Local Similarity 80.6% Pred No 2,1e-105;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 QY 5 AISPANDFLAGIAAISKTVAPTEIEVKLLLOVQASQIADKQVGYDVCIRIPE 64
 DB 20 AVEFVDFPAGGISAASVAKTAVTEIEVKLLLOVQASQIADKQVGYDVCIRIPE 79
 QY 65 QGVLSFWRGNLANVIRYPTQALNFAFKDKYKQITIGYDKITQWRIFAGNLSGGAAG 124
 DB 80 QGVLSFWRGNLANVIRYPTQALNFAFKDKYKQVFLGVGDKNTQWRIFAGNLSGGAAG 139
 QY 125 ATSLCEFYPLDFARTRLAADVKGSGTEREFGDCLVITKTSDEIRGLYOGFSVYQGI 184
 DB 140 ATSLCEFYPLDFARTRLAADYKGG-OREFTGLNCLTRIFKSDIVGLYRFGFSVYQGI 198
 QY 185 IITRAAFYGVYDIAKGLPDPKNTIIVSNMIAQTYTAAGVAVSPFTVRRMMOSGR 244
 DB 199 IITRAAFYGVYDIAKGLPDPKNTIIVSNMIAQTYTAAGVAVSPFTVRRMMOSGR 258
 QY 245 KGNADIMTGVDCWRKRFDEGKAFKAGMSVNLKMGAFVLVYDELKVI 298
 DB 259 KATVYIKNTLHKMTAKMTAKQESTGAFKAGMSVNLKMGAFVLVYDELKVI 312
 RESULT 13
 ID Q9NHW5 PRELIMINARY; PRT: 300 AA.
 Q9NHW5
 AC Q9NHW5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Fteiygota.
 CC Calliphoridae; Lucilla.
 NCBI_Taxid=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";
 CC Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: AF218587; AAF32322.1;
 DR InterPro: IPR001993; Mitochondrial carrier.
 DR InterPro: IPR002067; Mitochondrial carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCARRIER.
 KW Membrane; Transmembrane; Transport.
 SQ
 Query Match 80.1% Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5% Pred No 1e-103;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;
 QY 6 ISFAPKLAGIAAISKTVAPTEIEVKLLLOVQASQIADKQVGYDVCIRIPE 65
 DB 9 LGEVDFPAGGISAASVAKTAVTEIEVKLLLOVQASQIADKQVGYDVCIRIPE 68
 QY 66 GVLISFWRGNLANVIRYPTQALNFAFKDKYKQITIGYDKITQWRIFAGNLSGGAAG 125
 DB 69 GVLISFWRGNLANVIRYPTQALNFAFKDKYKQVFLGVGDKNTQWRIFAGNLSGGAAG 128
 QY 126 TSLCEFYPLDFARTRLAADVKGSGTEREFGDCLVITKTSDEIRGLYOGFSVYQGI 185

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Db 129 TSLCFYVPLDFAKRLADTKGG-QREFTGLNCLAKIFKSDGLVGLRGFVSVOGII 187
QY 186 IYRAAFGYVDTAKGMLDPKNTHTVSMIAQVTAVAGVSYPPDVTYRRMMQSGR 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 188 IYRAAFGFYDARGLPDPKNTPIYISWIAQVTVVAGVSYPPDVTYRRMMQSGR 247
QY 246 GADIMYTGVDGWRKIFRDEGKAFKFGKMSNVLRMGAFVLYLYDELAKYI 288
    :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 248 ATEIITYKNTLHCWATIAKQEGTGAFFKGAFSNVLRKGTGAFVLYLYDEIKKL 300

RESULT 14
ID 044093 PRELIMINARY; PRT; 288 AA.
AC 044093;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN ADP/ATP translocase (Fragment).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF025799; AAB87883.1; -.
DR FlyBase; Fggn0023292; Dpae\sesb.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr. 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
Best Local Similarity 80.7%; Pred. No. 2.2e-99;
Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISFADFLAGGIAAISKTAAPIRKVLLOVQHASKOIADKQYKGIQVDCIYRIPKE 64
    || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AIGFVADFAGGISAASVSTAVAPIRKVLLOVQHSKQISPDKQYKGVDCFIYRIPKE 66
QY 65 QGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGGA 124
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 QGFSSFWRGNLANVIRYPTQALNFAFKDKYKQVFLGVDKHTQFWRYFAGNLASGGA 126
QY 125 ATSLCFVYPLDFAKRLADTKGG-QREFTGLNCLAKIFKSDGLVGLRGFVSVOGI 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 ATSLCFVYPLDFAKRLADTKGG-QREFTGLNCLAKIFKSDGLVGLRGFVSVOGI 185
QY 185 IYRAAFGYVDTAKGMLDPKNTHTVSMIAQVTAVAGVSYPPDVTYRRMMQSGR 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 IYRAAFGFYDARGLPDPKNTPIYISWIAQVTVVAGVSYPPDVTYRRMMQSGR 244
QY 245 KGADIMYTGVDGWRKIFRDEGKAFKFGKMSNVLRMGAFVLY 289
    |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db 245 KATEIITYKNTLHCWATIAKQEGTGAFFKGAFSNVLRKGTGAFVLY 288

RESULT 15
ID 044094 PRELIMINARY; PRT; 288 AA.
AC 044094;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

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DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila subobscura (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF025799; AAB87884.1; -.
DR FlyBase; Fggn0023237; Dsub\sesb.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr. 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
Best Local Similarity 80.4%; Pred. No. 5e-99;
Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISFADFLAGGIAAISKTAAPIRKVLLOVQHASKOIADKQYKGIQVDCIYRIPKE 64
    |:| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AMGFVADFAGGISAASVSTAVAPIRKVLLOVQHSKQISPDKQYKGVDCFIYRIPKE 66
QY 65 QGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGGA 124
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 QGFSSFWRGNLANVIRYPTQALNFAFKDKYKQVFLGVDKHTQFWRYFAGNLASGGA 126
QY 125 ATSLCFVYPLDFAKRLADTKGG-QREFTGLNCLAKIFKSDGLVGLRGFVSVOGI 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 ATSLCFVYPLDFAKRLADTKGG-QREFTGLNCLAKIFKSDGLVGLRGFVSVOGI 185
QY 185 IYRAAFGYVDTAKGMLDPKNTHTVSMIAQVTAVAGVSYPPDVTYRRMMQSGR 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 IYRAAFGFYDARGLPDPKNTPIYISWIAQVTVVAGVSYPPDVTYRRMMQSGR 244
QY 245 KGADIMYTGVDGWRKIFRDEGKAFKFGKMSNVLRMGAFVLY 289
    |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db 245 KATEIITYKNTLHCWATIAKQEGTGAFFKGAFSNVLRKGTGAFVLY 288

Search completed: August 18, 2003, 16:13:48
Job time : 100 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:10:07 ; Search time 29 Seconds

(without alignments)
434.781 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQALSFRAKDFLAGGIAAA.....LRMGCAFVLYLDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	4	US-09-434-354-49 Sequence 49, Appl
2	1454	94.2	298	4	US-09-434-354-48 Sequence 48, Appl
3	1412	91.5	298	3	US-08-961-871-10 Sequence 10, Appl
4	1385.5	89.8	297	4	US-09-434-354-47 Sequence 47, Appl
5	314	20.3	469	4	US-09-996-243-289 Sequence 289, App
6	311	20.2	469	3	US-09-188-930-339 Sequence 339, App
7	311	20.2	469	4	US-09-312-283C-339 Sequence 339, App
8	286	18.5	335	4	US-09-482-273-118 Sequence 118, App
9	283.5	18.4	291	4	US-09-501-558-2 Sequence 2, Appl
10	280	18.1	447	4	US-09-160-119-4 Sequence 4, Appl
11	280	18.1	674	4	US-09-160-119-2 Sequence 2, Appl
12	265	17.2	312	3	US-09-142-565-2 Sequence 56, Appl
13	250.5	16.2	299	1	US-08-518-878B-56 Sequence 56, Appl
14	250.5	16.2	299	1	US-08-470-868A-55 Sequence 55, Appl
15	250.5	16.2	309	1	US-08-518-878B-51 Sequence 51, Appl
16	250.5	16.2	309	2	US-08-807-861A-51 Sequence 51, Appl
17	250.5	16.2	309	2	US-08-470-868A-51 Sequence 51, Appl
18	250.5	16.2	309	3	US-09-210-681-51 Sequence 51, Appl
19	250.5	16.2	309	3	US-08-946-719A-51 Sequence 51, Appl
20	250.5	16.2	309	4	US-09-547-983-51 Sequence 51, Appl
21	250.5	16.2	311	2	US-08-775-009-33 Sequence 33, Appl
22	245	15.9	432	2	US-08-937-466-4 Sequence 4, Appl
23	245	15.9	432	2	US-09-172-528-4 Sequence 4, Appl
24	245	15.9	432	3	US-09-318-199-4 Sequence 4, Appl
25	245	15.8	432	3	US-09-503-579-4 Sequence 4, Appl
26	244	15.8	308	2	US-08-937-466-2 Sequence 2, Appl
27	244	15.8	308	2	US-09-172-528-2 Sequence 2, Appl

28	244	15.8	308	3	US-09-318-199-2	Sequence 2, Appl
29	244	15.8	308	3	US-09-503-579-2	Sequence 2, Appl
30	243.5	15.8	311	2	US-08-775-009-32	Sequence 32, Appl
31	232.5	15.1	320	2	US-08-933-750C-12	Sequence 12, Appl
32	232.5	15.1	320	3	US-09-234-613-12	Sequence 12, Appl
33	227.5	14.7	303	1	US-08-294-522B-36	Sequence 36, Appl
34	226.5	14.7	303	1	US-08-518-878B-37	Sequence 37, Appl
35	226.5	14.7	303	2	US-08-807-861A-37	Sequence 37, Appl
36	226.5	14.7	303	3	US-08-470-868A-37	Sequence 37, Appl
37	226.5	14.7	303	3	US-09-210-681-37	Sequence 37, Appl
38	226.5	14.7	303	3	US-08-946-719A-37	Sequence 37, Appl
39	226.5	14.7	303	4	US-09-547-983-37	Sequence 37, Appl
40	222	14.4	293	4	US-09-501-558-4	Sequence 37, Appl
41	211	13.7	306	5	PCT-US94-09799-1	Sequence 4, Appl
42	205.5	13.3	307	2	US-08-807-861A-56	Sequence 56, Appl
43	205.5	13.3	307	3	US-09-210-681-56	Sequence 56, Appl
44	205.5	13.3	307	3	US-08-946-719A-56	Sequence 56, Appl
45	205.5	13.3	307	4	US-09-547-983-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-434-354-49
Sequence 49, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigieri, Luciano G.
APPLICANT: Velicel, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-49

Query Match 100.0%; Score 1543; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.5e-166;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEQALSFRAKDFLAGGIAAISTKTAAPFERKVLILQVQHASQIADQYKIVCIYR 60
DB	1	MTEQALSFRAKDFLAGGIAAISTKTAAPFERKVLILQVQHASQIADQYKIVCIYR 60
QY	61	IPKEQGVLSFWKRNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRPAGNIASG 120
DB	61	IPKEQGVLSFWKRNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRPAGNIASG 120
QY	121	GAAGATSLCFVYPLDFARFLADVGKSGTEREFGIGDCLVYTKRSDGIRGLYOGFSVS 180
DB	121	GAAGATSLCFVYPLDFARFLADVGKSGTEREFGIGDCLVYTKRSDGIRGLYOGFSVS 180
QY	181	VQGIIRYRAVFEVYDTAGKMLDPKNTHTIVVSMIAQVTVAVAGVSTPFDVRRRMM 240
DB	181	VQGIIRYRAVFEVYDTAGKMLDPKNTHTIVVSMIAQVTVAVAGVSTPFDVRRRMM 240
QY	241	QSGRKADIMYTGTVDCMKRIIFDEGKAFKFKAMSNVLRMGCAFVLYLDELKVI 298
DB	241	QSGRKADIMYTGTVDCMKRIIFDEGKAFKFKAMSNVLRMGCAFVLYLDELKVI 298

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RESULT 2
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wile, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Fritzel, Luciano G.
; APPLICANT: Velicel, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: 660088.433
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48

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Query Match          94.2%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 5,2e-156;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSPKADFLAGGIAAISKTRAVAPIERVKLLQVHASKQIADKQYKGIYDCIVR 60
DB 1 MTDALSPKADFLAGGIAAISKTRAVAPIERVKLLQVHASKQIADKQYKGIYDCIVR 60
QY 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCEFYPLDFARTRLADVGKSGTEREFGDGLVKTISDGIKGLYOGFSVS 180
DB 121 GAAGATSLCEFYPLDFARTRLADVGKSGTEREFGDGLVKTISDGIKGLYOGFSVS 180
QY 181 VOGIIRAAVFEVYDTAKGMLPDKNTHIVSMIAQVTAAGVVSYPEDTVARRMM 240
DB 181 VOGIIRAAVFEVYDTAKGMLPDKNTHIVSMIAQVTAAGVVSYPEDTVARRMM 240
QY 241 QSGRGADIMYTGTLDCMRKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELK 296
DB 241 QSGRGADIMYTGTLDCMRKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELK 296

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RESULT 3
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,871
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,017
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-871-10

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Query Match          91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2,9e-151;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQATSPKADFLAGGIAAISKTRAVAPIERVKLLQVHASKQIADKQYKGIYDCIVR 60
DB 1 MTDALSPKADFLAGGIAAISKTRAVAPIERVKLLQVHASKQIADKQYKGIYDCIVR 60
QY 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKEQGVSEFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCEFYPLDFARTRLADVGKSGTEREFGDGLVKTISDGIKGLYOGFSVS 180
DB 121 GAAGATSLCEFYPLDFARTRLADVGKSGTEREFGDGLVKTISDGIKGLYOGFSVS 180
QY 181 VOGIIRAAVFEVYDTAKGMLPDKNTHIVSMIAQVTAAGVVSYPEDTVARRMM 240
DB 181 VOGIIRAAVFEVYDTAKGMLPDKNTHIVSMIAQVTAAGVVSYPEDTVARRMM 240
QY 241 QSGRGADIMYTGTLDCMRKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELK 298
DB 241 QSGRGADIMYTGTLDCMRKIFRDEGKAFKFGAMSVNLKMGAFVLVYDELK 298

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RESULT 4
US-09-434-354-47
; Sequence 47, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wile, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Fritzel, Luciano G.
; APPLICANT: Velicel, Gonul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: 660088.433
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien

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us-09-811-094-33.ra1

Page 4

1	PRIOR FILING DATE: 1998-06-17
2	PRIOR APPLICATION NUMBER: 60/089599
3	PRIOR FILING DATE: 1998-06-17
4	PRIOR APPLICATION NUMBER: 60/089600
5	PRIOR FILING DATE: 1998-06-17
6	PRIOR APPLICATION NUMBER: 60/089653
7	PRIOR FILING DATE: 1998-06-17
8	PRIOR APPLICATION NUMBER: 60/089801
9	PRIOR FILING DATE: 1998-06-18
10	PRIOR APPLICATION NUMBER: 60/089907
11	PRIOR FILING DATE: 1998-06-18
12	PRIOR APPLICATION NUMBER: 60/089908
13	PRIOR FILING DATE: 1998-06-18
14	PRIOR APPLICATION NUMBER: 60/089947
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17	PRIOR FILING DATE: 1998-06-19
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22	PRIOR APPLICATION NUMBER: 60/090252
23	PRIOR FILING DATE: 1998-06-22
24	PRIOR APPLICATION NUMBER: 60/090254
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27	PRIOR FILING DATE: 1998-06-23
28	PRIOR APPLICATION NUMBER: 60/090355
29	PRIOR FILING DATE: 1998-06-23
30	PRIOR APPLICATION NUMBER: 60/090429
31	PRIOR FILING DATE: 1998-06-24
32	PRIOR APPLICATION NUMBER: 60/090431
33	PRIOR FILING DATE: 1998-06-24
34	PRIOR APPLICATION NUMBER: 60/090435
35	PRIOR FILING DATE: 1998-06-24
36	PRIOR APPLICATION NUMBER: 60/090444
37	PRIOR FILING DATE: 1998-06-24
38	PRIOR APPLICATION NUMBER: 60/090445
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46	PRIOR APPLICATION NUMBER: 60/090542
47	PRIOR FILING DATE: 1998-06-24
48	PRIOR APPLICATION NUMBER: 60/090557
49	PRIOR FILING DATE: 1998-06-24
50	PRIOR APPLICATION NUMBER: 60/090676
51	PRIOR FILING DATE: 1998-06-25
52	PRIOR APPLICATION NUMBER: 60/090678
53	PRIOR FILING DATE: 1998-06-25
54	PRIOR APPLICATION NUMBER: 60/090690
55	PRIOR FILING DATE: 1998-06-25
56	PRIOR APPLICATION NUMBER: 60/090694
57	PRIOR FILING DATE: 1998-06-25
58	PRIOR APPLICATION NUMBER: 60/090695
59	PRIOR FILING DATE: 1998-06-25
60	PRIOR APPLICATION NUMBER: 60/090696
61	PRIOR FILING DATE: 1998-06-25
62	PRIOR APPLICATION NUMBER: 60/090862
63	PRIOR FILING DATE: 1998-06-26
64	PRIOR APPLICATION NUMBER: 60/090863
65	PRIOR FILING DATE: 1998-06-26
66	PRIOR APPLICATION NUMBER: 60/091360
67	PRIOR FILING DATE: 1998-07-01
68	PRIOR APPLICATION NUMBER: 60/091478
69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091544
71	PRIOR FILING DATE: 1998-07-01
72	PRIOR APPLICATION NUMBER: 60/091519
73	PRIOR FILING DATE: 1998-07-02

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Best Local Similarity	30.1%;	Pred. No. 7.8e-27;		
Matches	89;	Conservative	60;	Mismatches 115;
				Indels 32;
				Gaps 11;

[illegible]

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RESULT 6
US-09-188-930-339
: Sequence 339, Application US/09188930A
: Patent No. 6150512
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Orrust, Rene
: APPLICANT: Morrison, James Greg
: TITLE OF INVENTION: Compositions Isolated
: TITLE OF INVENTION: and Methods For Their
: FILE REFERENCE: 11000.1011c1
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 339
: LENGTH: 469
: TYPE: PRT
: ORGANISM: Mouse
US-09-188-930-339

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[illegible]

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Db      297 SIIPMEVLITRMA--LRKGG---QXSGMDCARRIIAEGVAAEFKGIIIPMLGIIIPYAG   351
Oy      190 AFGGVYDTAKGLPDKNTHI-----VYSMTAQTIVTVAVG--VVSPTDPYRRR   237
        ||| |         ||| |::: |::: |::: |::: |::: |::: |::: |
Db      352 IDLAVYEI-----KNWLDORAVANSADPEVFLLACGIISTSCQGLASTPLALYRTR   406
Oy      238 MMMSGRKKADIMYTGYVDCCMRKITRDGSGRAFFEGMGSNVLRGMGAFA-VLYIDELK   295
        ::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |
Db      405 MAQAQSIECAPETVMSSL-FKOILRTSEAEGLYGCLAPNNMKYIIPAVISYVEYNLK   461
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RESULT 7
US-09-312-283C-339

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Sequence 339, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRF
ORGANISM: Mouse
US-09-312-283C-339

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Query Match	20.28;	Score 311;	DB 4;	Length 469;
Query Match	20.28;	Score 311;	DB 4;	Length 469;

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      23.4%, pred. NO. 1.e-26)
  desc. Local Similarity
Matches 88; Conservative 62; Mismatches 11; Indels 38; Gaps 11.

OY 10 KDLFAGGAAIASTPAVAPIERVKLLLOVHASKOIADKOYKGVDCIVRIPEKOGVLS 69
   : :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 188 RHLYAGGAGAVSRTCTAPLDRLVLMQV-HASR-----SNNMCTIVGPTQAIRGAGKS 241

OY 70 FMRGNANVIYFFPTQALNFAFKDKRYKQIFLGVDVKHTQFMRYPFAGNLSAGGAATSLC 129
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 242 LMRNGINVLKIAIESAKFMAYEDMKR--LVGSGQET---LRIHERLYAGSLAAIAQS 296

OY 130 FVYPLDPAARTPLAADVCKSGTEREERFGIDCLVLTIKSGDINGLGYQGSVSVOGIIITYRA 189
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 297 SIYPMEVLTATMA--LRKTK---QYSGMLDCAIRILAKEGVAAPFYKGIPTNMLGITTPAAG 351

OY 190 AYFGYVDLTAKMGLDPPKNTHL-----VYSMTAQIVTAAVG--VVSPEDTVRRR 237
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 352 IDLAVYEPL-----KATWLORYAVNSADGVEFLTLAGRTISSCGOLASYPALAVPTR 404

OY 238 MMQSGRGADIMYTGVDCKRKIFPRDGSKRAFFGAMSNNLRGCAFAV--LYLDELK 295
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 405 MQQAQSTIGAEVYMTSL--FKQILRTGAGLGLKPLNPEKVALPAVSISTVYENLK 461

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RESULT 8
US-09-482-273-118

Sequence 118, Application US/09482373
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
EARLIER FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921

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? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/092,922
? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/092,956
? EARLIER FILING DATE: 1998-07-15
? NUMBER OF SEQ ID NOS: 267
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 118
? LENGTH: 335
? TYPE: prt
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (335)
?: OTHER INFORMATION: xaa equals stop translation
US-09-462-273-118

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Query Match	18.5%;	Score 286;	DB 4;	Length 335;
Best Local Similarity	29.0%;	Pred. No. 6.9e-24;		
Matches	87;	Conservative	50;	Mismatches 133;
			Indels	30;
			Gaps	8

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QY      10 KDLAGIAAIASTKVAIEIRYKTKLLYQVNHAS-----KQJADKQYGVDCVIRLPRKE 64
Db      51 KPPVYGLASIAAEFTFPVDLTKRLQYQGSIDARKKEI-----KRGMHAFRICKE 106
QY      65 QCVLSTWRGNLANVIRFPYTOALNFAFDKKYKQIFLGGVDKHTQFWRIRFAGNLTASGGAAG 124
Db      107 EGVIALYSGIALPLRQASGYTKIKGIYQSLRKILFEVLEDEET-----LLIMMGCVVSG 161
QY      125 ATSLCFVYPLDFAFLRPLADVQKSGEHEFRFRLGDSGLVTKRSPGIRGLYQGSFVSQGI 184
Db      162 VISSTIANPVDYIKRIMQA-----QSSLQGSIMIGS-FIDLYQOESTKRLMGVPPYRQRA 216
QY      185 IIRRAAYFGVYDTAK-----GMLDPKNTHLIVSMMLAQVTVAAGVASYSPEDTVRRM 238
Db      217 AIYVGVELPYVDITKHLILISGMMDGJLILTHVSF-----TCGLAGALASNPVDVYVTRM 272
QY      239 MMSGGRKGDIMVTYGVDCMKRIIFDEGKAKAFPKAWSNVLR-GMGCAFVLYLYDELKAY 297
Db      273 MNDRAIVGNDVILKGVDSILKRMKHHEGFALYKKEFWNMLRLRPMNIIFFIYEQIKRL 332

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RESULT 9
US-09-501-558-2

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: Sequence 2, Application US/09501558
: Patent No. 6403784
:
: GENERAL INFORMATION:
:
: APPLICANT: Turner, C. Alexander Jr.
:
: APPLICANT: Mathur, Brian
:
: APPLICANT: zambrowicz, Brian
:
: APPLICANT: Sands, Arthur T.
:
: TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
: TITLE OF INVENTION: Polynucleotides Encoding the Same
:
: FILE REFERENCE: LEX-0012-USA
:
: CURRENT APPLICATION NUMBER: US/09/501,558
:
: CURRENT FILING DATE: 2000-02-09
:
: NUMBER OF SEQ ID NOS: 4
:
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO. 1

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ORGANISM: Homo sapiens
US-09-501-558-2

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Matches	87	Conservative	54	Mismatches	129
				Indels	31
				Gaps	9

Mon Aug 25 09:31:45 2003

us-09-811-094-33.ra1

Page 6

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Db      63  ECLIAALXSGIAPMLAQAASGVIKIGTYQSLKRIIFRPEDEI-----LPVIVIGILSG 117
Qy      125  ATSLCFYVPIEDFARTRLADVKGSGTEREFGIDCLVTKSGDGRIGYOGFSVQGI 184
Db      118  VISSTIANPFDVLRKMQA-----QSTIQ--GSMIGNFMNIYQOEGRGIMKGVSLFQA 172
Qy      165  IYRAAFVGYDTRK-----GMEDPKNTHIVSMIAQTVRAVAGVYSEPDVRRRM 238
Db      173  AIVGVLEPYDITKRLHLSIGMGDYITIFLSF-----TCGLAGALASNPVDVTRRM 228
Qy      239  MMQSG-RKQADIMYTGVDCKMRIRDEGKAFFRGKANSVLR-GMGAFAVYVIXDELK 296
Db      229  MNORVLRDGRSGVYTGIDCLQITMKNBSGFALYKGFPMNLRIGFMNIIFVYIEQLK 288
Qy      297  V 297
Db      289  L 289
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RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEM, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; EARLIER FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRF
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
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Query Match      18.1%; Score 280; DB 4; Length 447;
Best Local Similarity 27.1%; Pred. No. 5.1e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4  QAIISAKDFLAGIAAIAISKTAVAPIERKILLOVHASKQIADKQKGIYDCIVRIPK 63
Db      96  QVASEAYRFGISVAGAVAGATVYFDLVKTRMOKRSTSGFVGLMKNSEDFCKVLR 155
Qy      64  EGVLSFWKGNLANVIRYPTQALNFAFKDKYQIFL---GGVDKHTQFWIRFAGNLASG 120
Db      156  YEEFEGFLRGILPOLLGVAPEKAIKLVNDFVRDKFMHNDGSP-----LAAETLAG 207
Qy      121  GAAGATSLCFYVPIEDFARTRLADVKGSGTEREFGIDCLVTKSGDGRIGLYOGFSVS 180
Db      208  GCAGGSOVYITNPLEYKIRLOV-AGEITTGPRVSL-----SVVRDGEFGYIKAKAC 261
Qy      181  VOGIIRAAVFGVYDTRAKMLDPRKNTHTIVSMIAQTVYAV-AGVSYPPDVTRRRM 239
Db      262  FLRDIPIFSATYPPCYAHVAKASFANEDGVSPGSLLAGAIGAPASLVTADVITKR-- 319
Qy      240  MOSGRKQADIMYTGVDCKMRIRFDEGKAFFRGKANSVLRGMGAFVLYVDEL 294
Db      320  LQVAAAGQTTYSVYIDCFRKLIREGPKALMKGAGARVRSRPPQGVYLLTYEL 374
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEM, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; EARLIER FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRF
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
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Query Match      18.1%; Score 280; DB 4; Length 674;
Best Local Similarity 27.1%; Pred. No. 9.4e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

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Qy      64  EGVLSFWKGNLANVIRYPTQALNFAFKDKYQIFL---GGVDKHTQFWIRFAGNLASG 120
Db      383  YEEFEGFLRGILPOLLGVAPEKAIKLVNDFVRDKFMHNDGSP-----LAAETLAG 434
Qy      121  GAAGATSLCFYVPIEDFARTRLADVKGSGTEREFGIDCLVTKSGDGRIGLYOGFSVS 180
Db      435  GCAGGSOVYITNPLEYKIRLOV-AGEITTGPRVSL-----SVVRDGEFGYIKAKAC 488
Qy      181  VOGIIRAAVFGVYDTRAKMLDPRKNTHTIVSMIAQTVYAV-AGVSYPPDVTRRRM 239
Db      489  FLRDIPIFSATYPPCYAHVAKASFANEDGVSPGSLLAGAIGAPASLVTADVITKR-- 546
Qy      240  MOSGRKQADIMYTGVDCKMRIRFDEGKAFFRGKANSVLRGMGAFVLYVDEL 294
Db      547  LQVAAAGQTTYSVYIDCFRKLIREGPKALMKGAGARVRSRPPQGVYLLTYEL 601
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RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Kelly James Beasley
; APPLICANT: Lee James Beasley
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; EARLIER FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 9705305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRF
; ORGANISM: HOMO SAPIEN
US-09-142-565-2
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Best Local Similarity 27.1%; Pred. No. 1.5e-21;
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 DB 122 AVAOPPTVVVRFQAO-ARAGGGRYOSTVNAVYKTARREGFRGLMKGTSFNVARNALVN 180
 QY 189 AAYGVYDTRK-----GMLPDPKMTHTVSMMLAQVTVAACVSYPRDVTYRRMMQOS 242
 DB 181 CAELVYTDLTKDALMLKANIMTDLPCHTSAFGAGFCTVIAS---PDVYKTRYM--- 233
 QY 243 GRKGADIMYGTVDCKRKIFRDEGKAFKFGAMSNVLR-GMGAFVLVLYDELKRYI 298
 DB 234 --NSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRAL 288

RESULT 15
 US-08-518-878B-51
 ; Sequence 51, Application US/08518878B
 ; Patent No. 5702902

GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 TITILE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pennile & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/518,878B
 FILING DATE: 23-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-036
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-08-518-878B-51

Query Match 16.2%; Score 250.5; DB 1; Length 309;
 Best Local Similarity 24.9%; Pred. No. 6.3e-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

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 DB 17 FLAGTAAIAIDLTIFEDTAKVRLQIGESQGPVNAVYSAQIRGVMGTILIMRTIEGR 76
 QY 69 SFWRGNIAVIRYPTQALNFAFKDYKQIFLQGVDKHTQENRYFAGMLASGGAAGATSL 128
 DB 77 SLYNGIVAGLQROMSFASVRIGLDYSVKQPYTKG-SEHAS---IGSRLAGSTTGALAV 131
 QY 129 CFVYPLDFARTRLADVGKSTEREFRGLDCLVTKITKSDINGLXQGPSVSGCIIYR 188
 DB 132 AVAOPPTDVVKVRFQAO-ARAGGGRYOSTVNAVYKTARREGFRGLMKGTSFNVARNALVN 190
 QY 189 AAYGVYDTRK-----GMLPDPKMTHTVSMMLAQVTVAACVSYPRDVTYRRMMQOS 242
 DB 191 CALVYTYDILKDALMLKANIMTDDLPCHTSAFGAGFCTVIAS---PDVYKTRYM--- 243

QY 243 GRKGADIMYGTVDCKRKIFRDEGKAFKFGAMSNVLR-GMGAFVLVLYDELKRYI 298
 DB 244 --NSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRAL 298

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 Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 16:13:53 ; Search time 57 Seconds
(without alignments)
684.894 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGGIAAA.....LRMGCAFYVLYLDELKVI 298

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1543	100.0	298	9 US-09-811-094-33	Sequence 33, Appl
2	1543	100.0	298	9 US-09-810-644-33	Sequence 33, Appl
3	1543	100.0	298	10 US-09-185-904A-33	Sequence 32, Appl
4	1454	94.2	298	9 US-09-811-094-32	Sequence 32, Appl
5	1454	94.2	298	10 US-09-810-644-32	Sequence 32, Appl
6	1454	94.2	298	10 US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.8	297	9 US-09-811-094-31	Sequence 31, Appl
8	1385.5	89.8	297	9 US-09-810-644-31	Sequence 31, Appl
9	1385.5	89.8	297	10 US-09-185-904A-31	Sequence 31, Appl
10	760.5	49.3	318	10 US-09-801-368-252	Sequence 252, Appl
11	749.5	48.6	366	9 US-09-734-569-170	Sequence 170, Appl
12	737	47.8	308	15 US-10-128-714-3338	Sequence 3338, Appl
13	737	47.8	308	15 US-10-128-714-8338	Sequence 8338, Appl
14	734.5	47.6	381	12 US-10-141-478A-2	Sequence 2, Appl
15	686	44.5	677	12 US-10-259-165-192	Sequence 192, Appl

16	518	33.6	132	9 US-09-925-301-1459	Sequence 1459, Appl
17	423	27.4	87	9 US-09-864-761-36440	Sequence 36440, A
18	368	23.8	475	10 US-09-777-921A-4	Sequence 4, Appl1
19	368	23.8	477	10 US-09-777-921A-2	Sequence 2, Appl1
20	333.5	21.6	410	10 US-09-777-921A-5	Sequence 5, Appl1
21	314	20.3	469	9 US-09-989-722-289	Sequence 289, Appl
22	314	20.3	469	9 US-09-989-723-289	Sequence 289, Appl
23	314	20.3	469	9 US-09-989-729-289	Sequence 289, Appl
24	314	20.3	469	9 US-09-989-727-289	Sequence 289, Appl
25	314	20.3	469	10 US-09-989-732-289	Sequence 289, Appl
26	314	20.3	469	10 US-09-989-730-289	Sequence 289, Appl
27	314	20.3	469	10 US-09-991-073-289	Sequence 289, Appl
28	314	20.3	469	10 US-09-990-442-289	Sequence 289, Appl
29	314	20.3	469	10 US-09-991-163-289	Sequence 289, Appl
30	314	20.3	469	10 US-09-993-604-289	Sequence 289, Appl
31	314	20.3	469	10 US-09-990-456-289	Sequence 289, Appl
32	314	20.3	469	10 US-09-989-721-289	Sequence 289, Appl
33	314	20.3	469	10 US-09-992-598-289	Sequence 289, Appl
34	314	20.3	469	10 US-09-989-293A-289	Sequence 289, Appl
35	314	20.3	469	10 US-09-989-733-289	Sequence 289, Appl
36	314	20.3	469	10 US-09-990-444-289	Sequence 289, Appl
37	314	20.3	469	10 US-09-991-181-289	Sequence 289, Appl
38	314	20.3	469	10 US-09-989-730-289	Sequence 289, Appl
39	314	20.3	469	10 US-09-990-436-289	Sequence 289, Appl
40	314	20.3	469	10 US-09-993-687-289	Sequence 289, Appl
41	314	20.3	469	11 US-09-989-734-289	Sequence 289, Appl
42	314	20.3	469	11 US-09-997-653-289	Sequence 289, Appl
43	314	20.3	469	11 US-09-993-667-289	Sequence 289, Appl
44	314	20.3	469	11 US-09-997-428-289	Sequence 289, Appl
45	314	20.3	469	11 US-09-997-666-289	Sequence 289, Appl

ALIGNMENTS

US-09-811-094-33	Sequence 33, Application US/09811094
1	Sequence 33, Appl1
2	Patent No. US20010044144A1
3	GENERAL INFORMATION:
4	APPLICANT: Anderson, Christen M.
5	APPLICANT: Davis, Robert E.
6	APPLICANT: Clevenger, William
7	APPLICANT: Willey, Sandra Eileen
8	APPLICANT: Willey, Scott W.
9	APPLICANT: Szabo, Tomas R.
10	APPLICANT: Ghosh, Sumittra S.
11	APPLICANT: Moos, Walter H.
12	TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AMT),
13	TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
14	FILE REFERENCE: 660088.420D4
15	CURRENT APPLICATION NUMBER: US/09/811.094
16	CURRENT FILING DATE: 2001-03-14
17	NUMBER OF SEQ ID NOS: 37
18	SOFTWARE: FastSeq for Windows Version 3.0
19	SEQ ID NO 33
20	LENGTH: 298
21	TYPE: PRT
22	ORGANISM: Homo sapien
23	US-09-811-094-33
24	Query Match
25	Best Local Similarity 100.0%; Score 1543; DB 9; Length 298;
26	Matches 298; Conservattive 0; Mismatches 0; Indels 0; Gaps 0;
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Mon Aug 25 09:31:45 2003

us-09-811-094-33.rapb

Page 2

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DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGSKGTERRERGLGDCLYKTKSDGIRGLYOGFSVS 180
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DB 181 VOGIIIRAAVFGVYDTAKGMLDPKRNTHIVYVSMIAQVYTAAGVVSYPEDTVRRMM 240
OY 241 QSGRGADIMYTGTVCCMKRIFRDEGKAFKFGAMSNTLRGMCAGFVLYLYDELKRYI 298
DB 241 QSGRGADIMYTGTVCCMKRIFRDEGKAFKFGAMSNTLRGMCAGFVLYLYDELKRYI 298

RESULT 2

US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-33

Query Match 100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQATSPAKDFLAGGIAAATSKTAVAPIERVKLLQVOHASKQIADKQYKGIYDCIYR 60
DB 1 MTEQATSPAKDFLAGGIAAATSKTAVAPIERVKLLQVOHASKQIADKQYKGIYDCIYR 60
OY 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
DB 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFAFTRRLAADVGSKGTERRERGLGDCLYKTKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGSKGTERRERGLGDCLYKTKSDGIRGLYOGFSVS 180
OY 181 VOGIIIRAAVFGVYDTAKGMLDPKRNTHIVYVSMIAQVYTAAGVVSYPEDTVRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKGMLDPKRNTHIVYVSMIAQVYTAAGVVSYPEDTVRRMM 240
OY 241 QSGRGADIMYTGTVCCMKRIFRDEGKAFKFGAMSNTLRGMCAGFVLYLYDELKRYI 298
DB 241 QSGRGADIMYTGTVCCMKRIFRDEGKAFKFGAMSNTLRGMCAGFVLYLYDELKRYI 298

RESULT 3

US-09-185-904A-33
Sequence 33, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.

APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-33

Query Match 100.0%; Score 1543; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQATSPAKDFLAGGIAAATSKTAVAPIERVKLLQVOHASKQIADKQYKGIYDCIYR 60
DB 1 MTEQATSPAKDFLAGGIAAATSKTAVAPIERVKLLQVOHASKQIADKQYKGIYDCIYR 60
OY 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
DB 61 IPKQGVLSFMRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFAFTRRLAADVGSKGTERRERGLGDCLYKTKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGSKGTERRERGLGDCLYKTKSDGIRGLYOGFSVS 180
OY 181 VOGIIIRAAVFGVYDTAKGMLDPKRNTHIVYVSMIAQVYTAAGVVSYPEDTVRRMM 240
DB 181 VOGIIIRAAVFGVYDTAKGMLDPKRNTHIVYVSMIAQVYTAAGVVSYPEDTVRRMM 240
OY 241 QSGRGADIMYTGTVCCMKRIFRDEGKAFKFGAMSNTLRGMCAGFVLYLYDELKRYI 298
DB 241 QSGRGADIMYTGTVCCMKRIFRDEGKAFKFGAMSNTLRGMCAGFVLYLYDELKRYI 298

RESULT 4

US-09-811-094-32
Sequence 32, Application US/09811094
Patent No. US2001004414A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-32

Query Match 94.2%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 2e-147;

Mon Aug 25 09:31:45 2003

us-09-811-094-33.rapb

Page 4

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRF
ORGANISM: Homo sapien
US-09-811-094-31

Query Match
Best Local Similarity 89.8%; Score 1385.5; DB 9; Length 297;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSFANDFLAGGIAAISTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
1 MGDHANSFLKDFLAGAATAVASKTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
DB 1 MGDHANSFLKDFLAGAATAVASKTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
QY 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180
121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180
DB 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 179
QY 181 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 240
180 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 239
DB 180 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 239
QY 241 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 298
240 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 297
DB 240 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 297

RESULT 8
US-09-810-644-31
Sequence 31, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moser, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
FILE REFERENCE: 660088.420D3
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRF
ORGANISM: Homo sapien
US-09-810-644-31

Query Match
Best Local Similarity 89.8%; Score 1385.5; DB 9; Length 297;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSFANDFLAGGIAAISTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
1 MGDHANSFLKDFLAGAATAVASKTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
DB 1 MGDHANSFLKDFLAGAATAVASKTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
QY 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180
121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180
DB 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180

DB 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 179
QY 181 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 240
180 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 239
DB 180 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 239
QY 241 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 298
240 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 297
DB 240 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 297

RESULT 9
US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRF
ORGANISM: Homo sapien
US-09-185-904A-31

Query Match
Best Local Similarity 89.8%; Score 1385.5; DB 10; Length 297;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSFANDFLAGGIAAISTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
1 MGDHANSFLKDFLAGAATAVASKTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
DB 1 MGDHANSFLKDFLAGAATAVASKTAVAPRIERVKLLQVHASKOIADKQYKIVDCIVR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTOFMRFFAGNLSAG 120
QY 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180
121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 180
DB 121 GAAGTSLCFYVPLDFARTRLAADVGR-AQREFHGLDGLCITKSDGLRGLYGFVS 179
QY 181 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 240
180 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 239
DB 180 VOGIITIRAAVFGYDPAKMLPDPKNTHTVSMIAQTYAVAGVSPFDVRRRMM 239
QY 241 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 298
240 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 297
DB 240 QSGRKGADIMYTGVDCKRIKDEGAKAFKAGANSVLRGAGAFVLYLDELKVI 297

RESULT 10
US-09-801-366-252
Sequence 252, Application US/09801366
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary

```

1  APPLICANT: Milne, Todd
2  APPLICANT: No. US20020128250A1man, Thea
3  APPLICANT: Royer, John
4  APPLICANT: Salama, Sofie
5  APPLICANT: Sherman, Amir
6  APPLICANT: Silva, Jeff
7  APPLICANT: Summers, Eric
8  TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungl
9  FILE REFERENCE: 109272.147
10 CURRENT APPLICATION NUMBER: US/09/801,368
11 CURRENT FILING DATE: 2001-03-07
12 PRIOR APPLICATION NUMBER: US 09/487,558
13 PRIOR FILING DATE: 2000-01-19
14 PRIOR APPLICATION NUMBER: US 60/160,587
15 PRIOR FILING DATE: 1999-10-20
16 NUMBER OF SEQ ID NOS: 440
17 SOFTWARE: PatentIn version 3.0
18 SEQ ID NO 252
19 LENGTH: 318
20 TYPE: PRF
21 ORGANISM: Saccharomyces cerevisiae
22 US-09-801-368-252

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Query Match	Score	DB	Length
49.38;	760.5;	10;	318;

Best Local Similarity 53.7%; Pred. No. 4.4e-73;
Matches 159; Conservative 42; Mismatches 86; Indels 9; Gaps 5

0y 7SEKDFLNGGIAAISKTAVPAPRRVKKLLQVO-HASRCLAADBOYKGAYDCIAPRKQ 65
| | | | | : | | | | | : | | | | | : | | | | | :
Db 22 NPLIDFLMGGSAAVAKTASPPIERVKLLIQNOEMLKGTLDRIKYAGILDCFKTATQ 81

Oy 66 GTSFWRGLTANYIRYEPFOALNFAFKDKYKQITLGVVDKHTQEWRRFYFGNLASGGAAGA 125
 11 :
Db 82 GTSFSEWRGTANVIRYPFOALNFAFKDKIKAMF--GPKREEGAKWFFGNLASGGAAGA 139

Oy 126 TSLCFVYPLDFAARLAD--VKSQCTEREFRGLGDCLYKITKSGIRGLYQGFESVYQG 183
 Db 140 LSLFVYSLDYARRLADSKSKSGGAQFQNGLLDVYKTKLSGVAAGIRYRGFLPSVYG 199
 140 LSLFVYSLDYARRLADSKSKSGGAQFQNGLLDVYKTKLSGVAAGIRYRGFLPSVYG 199

Oy 184 IITYRAAFGVYDPAKG--MLPDRNTHIVYSMTAQTVAVAVGVSYPETTVRRMMMS 242
 : : : : : : : : : : : : : : : : : :
Oz 190 IVYRGLEFGMYDSLKPLLTGLSGEFLASFLGMVVTGATSCSYPIEDTVRRMMTS 259

Qy 243 GRRGADIMTGTVDWCWKTFRDEGGKAFKFGAMSNVLRGNGGAFVLYLDELKKVI 298
 1 - - - - - 11 - - - - - 11 - - - - - 11 - - - - -
 Qb 260 GQA---VYDGAEDCLRKIVAAEVSGLSEGGCGNIIIRFVAGAGVISMYYOLOMIL 312
 1 - - - - - 11 - - - - - 11 - - - - - 11 - - - - -

RESULT 11
US-09-734-569-170

```

; Sequence 170, Application US/09734569
; Patent No. US20020054816A1
; GENERAL INFORMATION:

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; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas

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; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette

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; APPLICANT:  Schmidt, Ralf-Michael
; APPLICANT:  Reski, Ralf
; TITLE OF INVENTION:  Moss genes from Physcomitrella patens encoding proteins

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1 FILE REFERENCE: BASF-NAE-1332-99-US
2
3 CURRENT APPLICATION NUMBER: US/09/734,569
4
5 CURRENT FILING DATE: 2001-05-24
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; SEQ ID NO 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-170

```

Query Match 48.6%; Score 749.5; DB 9; Length 386;

Best Local Similarity 53.4%; Pred. No. 8.6e-12;
Matches 157; Conservative 44; Mismatches 84; Indels 9; Gaps 5;

Oy	7	S	K	N	D	F	L	A	G	G	I	A	A	I	S	K	T	A	V	A	P	I	E	R	V	K	L	L	O	V	-	H	A	S	K	O	I	A	N	D	K	Q	K	G	I	V	D	C	I	V	R	I	P	K	E	G	65
Db	84	S	E	T	D	F	L	A	G	G	S	A	V	S	K	T	A	A	P	I	E	R	V	K	L	L	I	O	N	D	E	M	L	K	G	R	L	S	H	P	K	G	G	E	C	F	S	T	V	K	E	143					

QY 66GSLFWRCGLTANYIRYFFQALNFAFKDKYKQIQLGVDVKKHTQWRRYFAGNLASGGAAGA 125
 144 GMSLWRGCTANYIRYFFQALNFAFKDKFSLGKYKKK - DGYWKWFGNLASGGAAGA 202

Oy 126 TSLCFVYPLDFAERLADY---GKSGTREFRGLDCLVKITKSDGIRGLYGESVSQ 182
Db 203 SLLFVEILDYARLRANDAKSSKKGGGGRQFNLDVYKKTATDDIGLRYRGFAISCA 262

Oy 183 GIIIRYAFVGYDTAKG-MLPDKNTHIVSWMIAQIYTAVAGVSYPEDTVRRMMNQ 241
 | | | | | : | : |
Dd 263 GIIVRYGLVFGEIDSLKPVVLGNLEENFLASLFGWGTITIGAGIASLPDVTVRMMNT 322
 | | | | | : | : |

QY 242 SGRKGGADIMYTGIVDCWRRIFRDEGGKAFKFGANSNVLRGMGGAFVLYLYDELK 295

Db 323 SGGA---VKYNGSDPAFKOILAKEGAKSLPFGAGANIIILRAVAGVLSGDOLO 373

RESULT 12
US-10-128-714-3338

[illegible]

```

; AFFILIANT: nu, Weing
; AFFILIANT: Tishkoff, Daniel
; APPLICANT: zamudio, Carlos
; APPLICANT: Froshkin, Aleksey M

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CURRENT APPLICATION NUMBER: US/10/128, 1/4
 CURRENT FILING DATE: 2002-04-23
 PRIOR APPLICATION NUMBER: US 60/285,697
 PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 60/287,066
 PRIOR FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: US 60/295,890
 FILING DATE: 2001-05-05

PRIOR APPLICATION NUMBER: US 60/303, 899
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316, 362
 PRTINUMBER: 00010001

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;
; NUMBER OF SEQ ID NOS: 8603
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 3338
;

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; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3338

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0y 7SFAKDFLAGGIAAISKTAFAPIERVKLLQVHASKOTA--DKQYGIIVDLVRIPK 63

Db 7AFDPSFAVGVSAAVSKTAAPERIKLL--VQODEMTRAGRIDRKYGIIDERRTAQ 64

Oy 242 SGGKAGDLMYTGTVDCWRKIIFRDEGGAFFKAANSNVLGMGGAFVLYVEDELK 295
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Dd 323 SGGLA---VKYNGSMDAFKOILAKEDGAKSLFPKGACANITLRAVAGCVLSGTDLQ 373

RESULT 12
US-10-128-714-3338

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; Publication No. US20030119013A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Jiang, BO

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:
: APPLICANT: Tishkoff, Daniel
: APPLICANT: Zamudio, Carlos
: APPLICANT: Eroshkin, Alexey M
:

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1  ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
2  ;
3  ; TITLE OF INVENTION: Methods of Use
4  ;
5  ; FILE REFERENCE: 10182-018-999
6  ;

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: CURRENT FILING DATE: 2002-04-23
 : PRIOR APPLICATION NUMBER: US 60/285,697
 : PRIOR FILING DATE: 2001-04-23
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PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-31

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; SOFTWARE: PatentIn version 3.1
; SEO ID NO 3338
; LENGTH: 308

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ORGANISM: Aspergillus fumigatus
US-10-128-714-3338

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Matches 154; Conservative	47;	Mismatches 85;	Indels 12;	Gaps 6

7 AATDSEAVGGVSAVSKTAAAPERIKLL-VQNDDEMIRAGRDLRKYNIIDERRTAQ 64

APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 syngenta
SEQ ID NO 192
LENGTH: 677
TYPE: PRT
ORGANISM: Oryza sativa
US-10-259-165-192

Query Match 44.5%; Score 686; DB 12; Length 677;

Best Local Similarity 50.3%; Pred. No. 1.2e-64;

Matches 155; Conservative 43; Mismatches 88; Indels 22; Gaps 9;

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DB 430 TLKDEGVIALMRGNANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFWRFFAGNLASG 488
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DB 489 GAAGACSLFVYSLDYARTRLANDAKAAKKGGRQPNGLVDYRKTLASDGIAGLTPWIQ 548
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DB 549 HLPVLVS--LSNRGLYFGYDSLKPVLVGNLQD---NFLASFLGNGITIGAGLASYP 602
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DB 603 IDTVRRRMMSGGA--VKYNSLDAFRQIVAKGAKSLFRGAGANILRAVAGAVIAG 659
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DB 660 YDKIQVV 667

Search completed: August 18, 2003, 16:23:10
Job time : 59 secs

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